

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 18:47:50 ; Search time 1902.81 Seconds

(without alignments)
2644.453 Million cell updates/sec

Title: US-09-786-715-8

Perfect score: 618
Sequence: 1 MAVEBGQVIGVHTVDEMKL.....DDLQATIAKHAASVAAASS 123

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 segs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+pn.model -DEV=slp
-Q/cg2.1/USPTO.spool/US09786715.r/unat_11082003.150514.6035/app_query.fasta_1.1052
-DB=GenEmbl -QFWT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR.SCORE=pcr -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pcr -NORW=ext -HEA=SIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09786715.ecgn_1_15721_etunat_11082003.150514.6035 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_inu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	444	71.8	664	8 AF323593	AF323593 Prunus pe
2	442	71.5	665	8 AY170650	AY170650 Pisum sat
3	425	68.8	593	8 PSA319808	AJ319808 Pisum sat
4	423.5	68.5	603	8 RCTH10RXN	Z70677 R. communis
5	410	66.3	345	6 AX505468	AX505468 Sequence
6	410	66.3	480	8 AY088687	AY088687 Arabidops
7	410	66.3	497	8 ATTH10ARA	Z14084 A. thaliana
8	406	65.7	526	11 G73679	G73679 R2488R etio
9	406	65.7	601	8 OS092541	U92541 Oryza sativ
10	406	65.7	666	6 E08194	E08194 RPS13 gene
11	406	65.7	687	8 R1C7R	D21836 Oryza sativ
12	404	65.4	698	8 NTRRNA	X58537 N. tabacum m
13	401	64.9	345	8 AF483265	AF483265 Populus t
14	397	64.2	596	8 TA89762	AJ009762 Trillium
15	393	63.6	784	8 AY271308	AY271308 Citrus x
16	392	63.4	393	6 A48516	A48516 Sequence 4
17	392	63.4	437	8 AF420472	AF420472 Trillium
18	392	63.4	630	6 A48520	A48520 Sequence 8
19	392	63.4	630	8 TDAJ1903	AJ001903 Trillium
20	392	63.4	653	6 AR016869	AR016869 Sequence
21	392	63.4	653	6 AR020895	AR020895 Sequence
22	392	63.4	653	6 AR027218	AR027218 Sequence
23	392	63.4	653	6 AR038505	AR038505 Sequence
24	392	63.4	653	6 AR064647	AR064647 Sequence
25	392	63.4	653	6 AR067572	AR067572 Sequence
26	392	63.4	653	6 I38524	I38524 Sequence 10
27	392	63.4	653	6 I56899	I56899 Sequence 10
28	392	63.4	653	6 I59665	I59665 Sequence 10
29	392	63.4	653	6 I75192	I75192 Sequence 10
30	388.5	62.9	580	8 BNU59380	U59380 Brassica na
31	388	62.8	384	6 A48514	A48514 Sequence 2
32	388	62.8	659	6 A48519	A48519 Sequence 7
33	388	62.8	670	8 TATH10RDH	X69915 T. aestivum
34	383	62.0	366	6 AX654096	AX654096 Sequence
35	383	62.0	740	8 AB053294	AB053294 Oryza sat
36	380.5	61.6	360	6 AX505469	AX505469 Sequence
37	380.5	61.6	360	8 BT004710	BT004710 Arabidops
38	380.5	61.6	556	8 AK118542	AK118542 Arabidops
39	378	61.2	393	8 AF286593	AF286593 Trillium
40	378	61.2	629	8 TAE04845	AJ404845 Trillium
41	378	61.2	630	8 PSA310990	AJ310990 Pisum sat
42	377.5	61.1	642	8 ATTH10RD1	Z35473 A. thaliana
43	376	60.8	357	8 AY040028	AY040028 Arabidops
44	376	60.8	528	8 ATTH10RD4	Z35476 A. thaliana
45	376	60.8	530	8 AK118035	AK118035 Arabidops

ALIGNMENTS

RESULT 1

AF323593 664 bp mRNA linear PLN 02-NOV-2001
LOCUS AF323593
DEFINITION Prunus persica thiodexon h mRNA, complete cds.
ACCESSION AF323593
VERSION AF323593.1 GI:16588842
KEYWORDS
ORGANISM Prunus persica (peach)
SOURCE Prunus persica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
1 (bases 1 to 664)
Callahan,A.M., Morgens,P.H. and Cohen,R.A.
Isolation and initial characterization of cDNAs for mRNAs regulated
during peach fruit development
J. Am. Soc. Hortic. Sci. 118, 531-537 (1993)
2 (bases 1 to 664)
Callahan,A.M., Morgens,P.H., Cohen,R.A. and Scorza,R.
Regulation of peach gene expression in a peach/almond hybrid
Unpublished
3 (bases 1 to 664)
Callahan,A.M., Dunn,L.L. and Cohen,R.A.
Direct Submission
Submitted (22-NOV-2000) USDA-ARS, Appalachian Fruit Research
Station, 45 Wiltshire Rd., Kearneysville, WV 25430, USA
FEATURES
source
location/Qualifiers
1..664
/organism="Prunus persica"
/mol_type="mRNA"
/cultivar="B612615"
/db_xref="taxon:3760"
/clone="pcn306c"
/tissue_type="ripe fruit"
71..481
/codon_start=1
/product="thiodexon h"
/protein_id="AAI26915.1"
/db_xref="GI:16588843"
/translation="MAEENOVIGCHTQWAEQOLHKGNNKLLVVDFTASWCPKRL
IAPLIAELAKTPEVFLKYVDLRTVSEMGVEAMPFTFLKDKIVKVGAKKD
ELOIKVKKHVAANAASATSATATATATASA"
BASE COUNT 182 a 147 c 161 g 174 t
ORIGIN
Alignment Scores:
Pred. No.: 1.27e-41 Length: 664
Score: 444.00 Matches: 81
Percent Similarity: 84.03% Conservative: 19
Best Local Similarity: 68.07% Mismatches: 19
Query Match: 71.84% Indels: 0
Gaps: 0
US-09-786-715-8 (1-123) x AF323593 (1-664)
QY 5 GluGluGlyGlnValIleGlyValHisThyValAspGluTrpLysLeuGlnLeuGlnAsn 24
Db 77 GAGGAATCAAGTCAATCGCTGCGCACATCAAGCGTGGGAAGACACCTCCANAG 136
QY 25 AlAlAspSerLysLysLeuIleValAlAspPheThrAlaSerTrpCysGlyProCys 44
Db 137 GGAACGAGAACAAAGAACTGGTGGTGGATTCACGCGCTTCTGGTGGACCGTGC 196
QY 45 ArgPheMetAlaProValIleuAlaGluIleAlaLysLysThrProGluLeuIlePheLeu 64
Db 197 CGGTTGATGCCCAATCTTGGCGAGTGGCTAAGAAAGCCAGAACGATGCTTCTTA 256
QY 65 LysValAspValAspGluValArgProValAlaGluGluTrpSerIleGluAlaMetPro 84
Db 257 AAGGTGACGTGATGATGAGACGCTTCCAGAGAGTGGGTGGTGGAGCAATGCTT 316
QY 85 ThrPheLeuPheLeuLysAspGlyGluIleValAlaLysLysValValGlyAlaSerLysAsp 104
Db 317 ACCTTCCTCTTCTCAAGGAAGCAAGATGATGACAAAGGTTGGTGGCCAGAAAGAC 376

QY 105 AspleuginaIatThrIleAlaLysHisAlaSerAlaValAlaAlaSerSerSer 123
Db 377 GAGTTACGATCAAGATTCGCCACACATGTCGCCCTGGCGGCTGCTCCGCCACC 433
RESULT 2
LOCUS AY170650 665 bp mRNA linear PLN 02-JAN-2003
DEFINITION Pisum sativum clone 3 thiodexon h mRNA, complete cds.
ACCESSION AY170650
VERSION AY170650.1 GI:27466893
KEYWORDS
ORGANISM Pisum sativum (pea)
SOURCE Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
Pisum.
1 (bases 1 to 665)
Montichard,F., Renard,M., Duval,F.D. and MachereJ,D.
Expression of the NADP-thiodexon reductase/thiodexons h system
during germination of seeds of Pisum sativum L
Unpublished
2 (bases 1 to 665)
Montichard,F., Renard,M., Duval,F.D. and MachereJ,D.
Direct Submission
Submitted (30-OCT-2002) UMR 1191 Physiologie Molculaire des
Semences, UFR Sciences, 16 bd Lavoisier, Angers 49045, France
FEATURES
source
location/Qualifiers
1..665
/organism="Pisum sativum"
/mol_type="mRNA"
/db_xref="taxon:3888"
/clone="3"
74..415
/note="trix h"
/codon_start=1
/product="thiodexon h"
/protein_id="AAO12854.1"
/db_xref="GI:27466894"
/translation="MAEEOVIGVHTVDANKLEQEKASKKLIVDFTSWCGPCRF
IAPLIAELAKTIVTFLKYVDLRTVSEMGVEAMPFTFLKDKELVKKVGAKKE
ELOIKDKHNA"
BASE COUNT 220 a 85 c 164 g 196 t
ORIGIN
Alignment Scores:
Pred. No.: 2.15e-41 Length: 665
Score: 442.00 Matches: 84
Percent Similarity: 86.49% Conservative: 12
Best Local Similarity: 75.68% Mismatches: 15
Query Match: 71.52% Indels: 0
Gaps: 0
US-09-786-715-8 (1-123) x AY170650 (1-665)
QY 5 GluGluGlyGlnValIleGlyValHisThyValAspGluTrpLysLeuGlnLeuGlnAsn 24
Db 80 GAAGAGGAGCAAGATCGGTGTCACACCGTGGATGCTGGAGGAAGAGTTAGAGAAG 139
QY 25 AlAlAspSerLysLysLeuIleValAlAspPheThrAlaSerTrpCysGlyProCys 44
Db 140 GGAAGACCCCAAGAAAGATGATGATGATTCACCTGCTTCTGGTGGCTCCATGC 199
QY 45 ArgPheMetAlaProValIleuAlaGluIleAlaLysLysThrProGluLeuIlePheLeu 64
Db 200 CGTTTATGCCCCAATTTTGGCAGAGATTGCTTAAAGCTTACATGTCATTTCTT 259
QY 65 LysValAspValAspGluValArgProValAlaGluGluTrpSerIleGluAlaMetPro 84
Db 260 AAGGTGACGTGATGATGATGAGACGCTTCCAGAGAGTGGGCAATGGAAGCTATGCCA 319
QY 85 ThrPheLeuPheLeuLysAspGlyGluIleValAlaLysLysValValGlyAlaSerLysAsp 104

DB 320 ACATCTGTTCTTCTGAAGATGTCGACTGTGCAGCAAGTGTGGTCCAGAGAGAG 379
QY 105 Aspleuginalathrilialalyshtsalaser 115
DB 380 GAGCTGCAATTCGAAATTCAGACATGTCAGCT 412

RESULT 3
PSA319808
LOCUS PSA319808 593 bp mRNA linear PLN 17-JUN-2001
DEFINITION Pisum sativum mRNA for thioedoxin h (trxx gene).
ACCESSION AJ319808
VERSION AJ319808.1 GI:14485508
KEYWORDS thioedoxin h; trxx gene.
SOURCE Pisum sativum (pea)
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.

REFERENCE 1
AUTHORS Navarro,E., Gomez,J.M., Jimenez,A. and Sevilla,F.
TITLE Isolation of a new thioedoxin h in pea plants. Expression during developmental and under oxidative stress induced conditions
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 593)
AUTHORS Navarro,E.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-2001) Navarro E., Nutrition and Plant Physiology, Cebas-csic, Cebas, Campus de Espinardo, Murcia, 30100, SPAIN

FEATURES
source
1..593
location/Qualifiers
/organism="Pisum sativum"
/mol_type="mRNA"
/db_xref="taxon:3888"
/tissue_type="leaves"
1..593
/gene="trxx"
60..416
/gene="trxx"
/codon_start=1
/product="thioedoxin h"
/protein_id="CAC42084.1"
/db_xref="GI:14485509"
/translation="MAENEVIAHSDSKKEQIOKTESKKLIIVDFTSKCGPCRF
IAPFLAEIAKRPVIFLKVDELKVAHEWVESMPTFLLKEGMEVDVYGAKE
ELQIAITKHTATVATA"

BASE COUNT 200 a 97 c 136 g 160 t
ORIGIN

Alignment Scores:
Pred. No.: 1.65e-39 Length: 593
Score: 425.00 Matches: 80
Percent Similarity: 83.48% Conservative: 16
Best Local Similarity: 69.57% Mismatches: 19
Query Match: 68.77% Indels: 0
Gaps: 0

US-09-786-715-8 (1-123) x PSA319808 (1-593)

QY 6 GIUGIUGIValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsn 25
DB 69 GAAATGAGGTGATCGCTTCATTCATCCATGATGAGAGAGACAGATCCAGAAAGCA 128
QY 26 LysAspSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCysArg 45
DB 129 ACCGATCCAAAAAAGTGTGTGATTTTACTGCTGCTGCTGCGTCCATGCGCT 188
QY 46 PheMetAlaProValLeuAlaGluIleAlaLysLysTrpProGluLeuIlePheLeuLys 65
DB 189 TTTATTGCTCAATTCCTTACAGAGATGCTTAAAGACACCTCAAGTATCTTCTCAAG 248
QY 66 ValAspValAspGluValArgProValAlaGluGluTrpSerIleGluAlaMetProThr 85

DB 249 GTGACATTTAGAGATTTAGAGAGTGTTCGCCAGAGATGTCTATGAGAGCTATGCCACC 308
QY 86 PheLeuPheLeuLysAspGlyGluIleValAlaAspLysValAlaGlyAlaSerLysAsp 105
DB 309 TTTCTGCTCTTGAAGAAGAGCATGGAAGGATGATGAGTGTGCTTGAAGAAGAGAA 368

QY 106 LeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAla 120
DB 369 CTGACGCTGGCAATACCAAGCATGACACACTGTTGCTACTGCT 413

RESULT 4
RCHIORXN
LOCUS RCHIORXN 603 bp mRNA linear PLN 04-APR-1996
DEFINITION R. communis mRNA for thioedoxin.
ACCESSION Z70677
VERSION Z70677.1 GI:1255953
KEYWORDS thioedoxin.
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.

REFERENCE 1 (bases 1 to 603)
AUTHORS Szederkényi,J., Dolgener,E. and Schobert,C.
TITLE cDNA expressed in Ricinus cotyledons
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 603)
AUTHORS Dolgener,E.
TITLE Direct Submission
JOURNAL Submitted (04-APR-1996) Dolgener E., University of Bayreuth, Department of Plant Physiology, Universitaetsstr.30, Bayreuth, Germany, 95440

FEATURES
source
1..603
location/Qualifiers
/organism="Ricinus communis"
/mol_type="mRNA"
/cultivar="Sanguineus"
/db_xref="taxon:3988"
/clone="PEDRH018"
/tissue_type="cotyledon"
/clone_lib="lambda Ecxell"
/dev_stage="seedling"
23..379
/codon_start=1
/product="thioedoxin"
/protein_id="CAA94534.1"
/db_xref="GI:1255954"
/db_xref="SPTREMBL:Q43636"
/translation="MAEEGVYIGCHTVEANNDLOKNDTRKGLIVDFTSKCGPCR
FIAPFLAEIAKRPVIFLKVDELKVAHEWVESMPTFLLKEGKIMDKVYGAKE
DELQOTIRKHTATVAST"

BASE COUNT 179 a 101 c 157 g 166 t
ORIGIN

Alignment Scores:
Pred. No.: 2.49e-39 Length: 603
Score: 423.50 Matches: 80
Percent Similarity: 83.05% Conservative: 18
Best Local Similarity: 67.80% Mismatches: 17
Query Match: 68.53% Indels: 3
Gaps: 1

US-09-786-715-8 (1-123) x RCHIORXN (1-603)

QY 5 GIUGIUGIValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsn 24
DB 32 GAAGAAGGCAAGTATGCGGTGCCACACTGTGAGCATGATGACATTCAGAGAG 91
QY 25 AlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCys 44
DB 92 GAAATGATMACCAAGAGCATGCTGTTGATTTTACTGCTCATGCTGAGACCATGC 151

```

QY 45 ArgPheMetAlaProValIleuAlaGluIleAlaLysThrProGluIlePheLeu 64
    ::::::::::::::::::::
Db 152 CGTTTCATGCTCCCTTCCTGCTGAGCTGCGCAAGAAACATGCAATGTTACTCTCGT 211

QY 65 LysValAspValAspGluValArgProValAlaGluIleuLysSerIleGluAlaMetPro 84
    ::::::::::::::::::::
Db 212 AAGGTGATGTGGATGATGATGAGACATGCTGCTACAGTGGCTGGAGTCAATGCCA 271

QY 85 ThrPheLeuPheLeuLysAspGluIleValAspLysValAlaGluAlaSerLysAsp 104
    ::::::::::::::::::::
Db 272 ACCTTATGTTCTCGAAGGAGGAGGAGATGATGACAAAGTGGTGGAGCAAGAAAGAC 331

QY 105 AspleuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAlaSerSer 122
    ::::::::::::::::::::
Db 332 GAATCGACGACAACTATGCGCAACAC-----ATGGCTACTGCTTCACAT 376

RESULT 5
AX505468 345 bp DNA linear PAT 27-SEP-2002
LOCUS Sequence 163 from Patent WO0216655.
ACCESSION AX505468
VERSION AX505468.1 GI:23386705
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
            Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
AUTHORS Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
TITLE Stress-regulated genes of plants: transgenic plants containing
JOURNAL same, and methods of use
        Patent: WO 0216655-A 163 28-FEB-2002;
        The Scripps Research Institute (US) ; Syngenta Participations AG
        (CH)
FEATURES
    source          Location/Qualifiers
                    1..345
                    /organism="Arabidopsis thaliana"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:3702"
BASE COUNT 90 a 68 c 90 g 97 t
ORIGIN
Alignment Scores: 4.47e-38 Length: 345
Pred. No.: 410.00 Matches: 73
Score: 85.32% Conservative: 20
Percent Similarity: 66.97% Mismatches: 16
Best Local Similarity: 66.34% Indels: 0
Query Match: 6 Gaps: 0
DB:
US-09-786-715-8 (1-123) x AX505468 (1-345)
QY 5 GluGluGluGluValIleGluValHisThrValAspGluThrPheLysLeuGluAsn 24
    ::::::::::::::::::::
Db 10 GAAGAGGACAGAGGATGCGCTGCGCACCGTTGAGCAAGACGACGCTTCAGAG 69

QY 25 AlaLysAspSerLysLysLeuIleValAlaAspPheThrAlaSerTPCysGlyProCys 44
    ::::::::::::::::::::
Db 70 GCTAATGATCCAAAACACTCTTGTGCTGTTGATTCACGCTTCTTGTGTGACCATGT 129

QY 45 ArgPheMetAlaProValIleuAlaGluIleAlaLysThrProGluIlePheLeu 64
    ::::::::::::::::::::
Db 130 CGTTTCATGCTCCCTTCCTGCTGATGCTGCTAAGCAACCTCTTACGCTTCTTC 189

QY 65 LysValAspValAspGluValArgProValAlaGluIleuLysSerIleGluAlaMetPro 84
    ::::::::::::::::::::
Db 190 AAGGTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249

QY 85 ThrPheLeuPheLeuLysAspGluIleValAlaSerLysValAlaGluAlaSerLysAsp 104
    ::::::::::::::::::::
Db 250 ACCTTATGTTCTTCGAAAGGAGGAGATTTTGGACAAAGTTTGGAGCAAGAAAGAT 309

```

```

QY 105 AspleuGlnAlaThrIleAlaLysHis 113
    ::::::::::::::::::::
Db 310 GAGCTTCAGTCTACCATTCGCAACAC 336

RESULT 6
AY088687 480 bp mRNA linear PLN 14-APR-2003
LOCUS Arabidopsis thaliana clone 9189 mRNA, complete sequence.
ACCESSION AY088687
VERSION AY088687.1 GI:21407461
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
            Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
            1 (bases 1 to 480)
REFERENCE
AUTHORS Haas, B.J., Volkovskiy, N., Town, C.D., Troukhan, M., Alexandrov, N.,
            Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
TITLE Full-length messenger RNA sequences greatly improve genome
JOURNAL annotation
        Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE 22088475
PUBMED 12093376
REFERENCE
AUTHORS Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
            Feldmann, K.
TITLE Full-length cDNA from Arabidopsis thaliana
JOURNAL Unpublished
REFERENCE
AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
            Feldmann, K.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
        Malibu, CA 90265, USA
COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made
        available to TIGR and Genbank. The following quality assessment of
        this set was done by comparison with known proteins: two percent of
        the clones are estimated to be 5'-truncated; less than one percent
        are 3'-truncated; approximately two percent represent alternative
        splice variants, including unspliced introns and spliced exons; one
        percent may contain premature stop codons; five percent may have
        frame shifts in a coding region. A sequence is considered to be
        5'-truncated if it lacks the translation initiation start (AUG). A
        sequence is considered to be 3'-truncated if it lacks the
        C-terminal end of the encoded protein. Please note that these cDNA
        sequences are derived from the Ws or Ilwr ecotypes and therefore
        may contain polymorphisms when compared to sequences from Col-0.
        Geneset carried out the library production and sequencing of the
        full-length clones. Ceres, Inc. carried out the clustering of the
        5' sequences, selection of clones, and sequence assembly.
FEATURES
    source          Location/Qualifiers
                    1..480
                    /organism="Arabidopsis thaliana"
                    /mol_type="mRNA"
                    /db_xref="taxon:3702"
                    /clone="9189"
                    13..357
                    /product="thioredoxin h"
                    /protein_id="AA067008.1"
                    /db_xref="GI:21617958"
                    /translation="MASEGVQACHTETVENEDLOKANESKTLVVVDFTASGCGPCR
                    FIAPFADLAKRLKPNVLFKVDDELKSVASDVAIDAMPFMFLKGGKIDKVVYGAKK
                    DEQSTIRAKLA"
BASE COUNT 124 a 93 c 111 g 152 t
ORIGIN
Alignment Scores: 6.64e-38 Length: 480
Pred. No.: 410.00 Matches: 73
Score: 85.32% Conservative: 20
Percent Similarity: 66.97% Mismatches: 16
Best Local Similarity:

```


Query Match: 66.34% Indels: 0
DB: 8 Gaps: 0

US-09-786-715-8 (1-123) x AT088687 (1-480)

QY 5 GtuglglglnVallelelglYvalHsthRvalAspGluTrpLysLeuGlnAsn 24
|||||
DB 22 GAAGAAGACAGTATGATCCCGCCACACCGTTGACATGAGACAGACGCTTCAAG 81
QY 25 AlAlysAspSerLysLysLeuLeleValAlAspPheThAlaSerTrpCysGlyProCys 44
|||||
DB 82 GCTAATGAATCCAAACCTCTGTGGTGAATTCACGCGCTTCTTGGTGAGACATGT 141
QY 45 ArgPheMetAlaProValLeuAlaGluLeleAlaLysLysThProGluLeuLePheLeu 64
|||||
DB 142 GCTTTCATCGCTCCATCTCTTGTGGTGAATTCACGCGCTTCTTGGTGAGACATGT 201
QY 65 LysValAspValAspGluValArgProValAlaGluGluTrpSerLeuAlaMetPro 84
|||||
DB 202 AAGGTTGATACGATGATGAATGAGTCGGTGCACAGTATGGCGATACAGCGATGCCA 261
QY 85 ThrPheLeuPheLeuLysAspGlyGluLeleValAlAspLysValAlGlyAlaSerLysAsp 104
|||||
DB 262 ACCCTTCATGCTTTTGAAGAGAGAAAGATTGTGACAAAGTTGAGACCAAGAAAGAT 321
QY 105 AspleuGlnAlaThrleAlaLysHts 113
|||||
DB 322 GAGCTTCAGCTACCATTCGCCAAGACAC 348

RESULT 7
ATTHIOARA 497 bp mRNA linear PLN 16-JUN-1994
LOCUS A.thaliana mRNA for thioredoxin H.
ACCESSION Z14084.1 GI:16551

VERSION Z14084.1
KEYWORDS thioredoxin H.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Rosids; eudots; II; Brassicales; Brassicaceae; Arabidopsis.
TITLE 1 (bases 1 to 497)
Nucleotide sequence of a cDNA clone encoding an Arabidopsis

JOURNAL thaliana thioredoxin h
MEDLINE Plant Physiol. 102 (1), 327-328 (1993)
PUBMED 94151431

REFERENCE
AUTHORS Meyer Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-1992) Yves Meyer PhD, Laboratoire de Physiologie

vegetale, Université de Perpignan, Av de Villeneuve 52, Perpignan,
66860, FRANCE

FEATURES

source
1. 497
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
30. 374
/codon_start=1
/product="thioredoxin H"
/protein_id="CA78462.1"
/db_xref="GI:16551"
/db_xref="SWISS-PROT:P29448"
/translation="MASEGQVIACTVEFWNEQLOKANESKTLVVDFTSWCGPCR
FIAPFADIAKKLPVLFPLKVDDELKSVADWAIQAMPFTMLEKGLDKVYGAKK
DELOSTIKKHLA"

BASE COUNT 135 a 94 c 116 g 152 t
ORIGIN

Alignment Scores: 6.92e-38 Length: 497
Pred. No.:

Score: 410.00
Percent Similarity: 85.32%
Best Local Similarity: 66.97%
Query Match: 66.34%
DB: 8 Gaps: 0

US-09-786-715-8 (1-123) x ATTHIOARA (1-497)

QY 5 GtuglglglnVallelelglYvalHsthRvalAspGluTrpLysLeuGlnAsn 24
|||||
DB 39 GAAGAAGACAGTATGATCCCGCCACACCGTTGACATGAGACAGACGCTTCAAG 98
QY 25 AlAlysAspSerLysLysLeuLeleValAlAspPheThAlaSerTrpCysGlyProCys 44
|||||
DB 99 GCTAATGAATCCAAACCTCTGTGGTGAATTCACGCGCTTCTTGGTGAGACATGT 158
QY 45 ArgPheMetAlaProValLeuAlaGluLeleAlaLysLysThProGluLeuLePheLeu 64
|||||
DB 159 GCTTTCATCGCTCCATCTCTTGTGGTGAATTCACGCGCTTCTTGGTGAGACATGT 218
QY 65 LysValAspValAspGluValArgProValAlaGluGluTrpSerLeuAlaMetPro 84
|||||
DB 219 AAGGTTGATACGATGATGAATGAGTCGGTGCACAGTATGGCGATACAGCGATGCCA 278
QY 85 ThrPheLeuPheLeuLysAspGlyGluLeleValAlAspLysValAlGlyAlaSerLysAsp 104
|||||
DB 279 ACCCTTCATGCTTTTGAAGAGAGAAAGATTGTGACAAAGTTGAGACCAAGAAAGAT 338
QY 105 AspleuGlnAlaThrleAlaLysHts 113
|||||
DB 339 GAGCTTCAGCTACCATTCGCCAAGACAC 365

RESULT 8
LOCUS G73679 526 bp DNA linear STS 16-JUL-2002
DEFINITION RZ488R etiolated leaf tissue of rice Oryza sativa STS genomic clone
RZ488 sequencing direction=reverse, sequence tagged site.

ACCESSION G73679.1 GI:19697274
VERSION G73679.1
KEYWORDS Oryza sativa (indica cultivar-group)
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
AUTHORS Euharioldae; Oryzaceae; Oryza.
TITLE 1 (bases 1 to 526)
JOURNAL McCouch, S. R.
COMMENT Unpublished (2002)

Contact: Susan R. McCouch
Cornell University
Dept. of Plant Breeding, Ithaca, NY 14853-1901, USA
Tel: 6072550420
Fax: 6072556683
Email: srm4@cornell.edu
Primer A: M13 universal Forward GTAAACGACGGCCAGT
Primer B: M13 universal Reverse AACACCTATGACCAAG
STS size: 526
Protocol:

Template: 20-100ng
Primer: 5pmol each
DNTPs: 40nmol
Tag polymerase: 5units
Total volume: 50ul

Buffer:
Tris-HCl: 100mM
KCl: 50mM
MgCl2: 15mM
Gelatin: 0.1%
pH: 8.3

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 686)	Kavano, M.	SIEVE TUBE PROTEIN GENE OF PLANT AND METHOD FOR MAKING USEFUL PROTEIN TRANSMIGRATE TO SIEVE TUBE USING THE SAME	Patent: JP 1994269286-A 1 27-SEP-1994;	
			MITSUI GIYOUSAI SHOKUBUTSU BIO KENKYUSHO:KK	
OS		Oryza sativa L., var. alchiasahi		
PN		JP 1994269286-A/1		
PD		27-SEP-1994		
PF		19-MAR-1993 JP 1993060763		
PI		KAYANO MITSUO		
PC		C12N15/29, A01H5/00, C12P21/02, //C12N5/10;		
CC		strandedness: Double;		
CC		topology: Linear;		
CC		feature is identified by other;		
key		Location/Qualifiers		
source		1..686		
FT		/organism='Oryza sativa L., var. alchiasahi'		
FT		/tisue='leaf'		
FT		/clone='CRSP13-1'		
FT		1..56		
FT		5'UTR		
FT		57..425		
FT		CDS		
FT		/product='sieve tube protein' FT		
FEATURES		426..686		
source		Location/Qualifiers		
1..686		/organism='unidentified'		
/mol_type='genomic RNA'		/db_xref='taxon:32644'		
BASE COUNT		170 a 150 c 182 g 184 t		
ORIGIN				
Alignment Scores:				
Score:		2.92e-37		
Percent Similarity:		406.00		
Best Local Similarity:		78.99%		
Query Match:		63.03%		
DB:		65.70%		
		Gaps:		
		6		
		0		
US-09-786-715-8 (1-123) x E08194 (1-686)				
QY		5		
Db		66		
QY		25		
Db		126		
QY		45		
Db		186		
QY		65		
Db		246		
QY		85		
Db		306		
QY		105		
Db		366		
RESULT 11				
RICHT		687 bp		
LOCUS		Oryza sativa (japonica cultivar-group) mRNA for thioresdoxin h,		
DEFINITION		complete cds.		
ACCESSION		D21836		

VERSION	D21836.1	GI:426441
KEYWORDS		
SOURCE		
ORGANISM	Oryza sativa (japonica cultivar-group)	
	Oryza sativa (japonica cultivar-group)	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
	Ehretodiaceae; Oryzaceae; Oryza.	
REFERENCE	1 (bases 1 to 687)	
AUTHORS	Ishiwatari,Y., Honda,C., Kawashima,I., Nakamura,S., Hirano,H.,	
	Mori,S., Fujiwara,T., Hayashi,H. and Chino,M.	
	Thioredoxin h is one of the major proteins in rice phloem sap	
	Planta 195 (3), 456-463 (1995)	
JOURNAL	95218606	
MEDLINE	7/66047	
PUBMED	2 (bases 1 to 687)	
REFERENCE	Ishiwatari,Y.	
AUTHORS	Direct Submission	
TITLE	Submitted (28-OCT-1993) Yutaka Ishiwatari, The university of Tokyo,	
JOURNAL	Faculty of Agriculture, Department of Agricultural Chemistry; 1-1-1,	
	Yayoi, Bunkyo-ku, Tokyo 113, Japan (Tel:81-3-3812-2111(ex.5105),	
	Fax:81-3-3812-0544)	
	Location/Qualifiers	
FEATURES	1..687	
source	/organism="Oryza sativa (japonica cultivar-group)"	
	/mol_type="mRNA"	
	/cultivar="Nipponbare"	
	/db_xref="taxon:39947"	
	/clone_lib="library of Dr.D. Shibata"	
	/note="clones cRPS13-312 and cRPS13-322"	
	57..425	
	/note="encoding rice phloem sap 13kd protein-1"	
	/codon_start=1	
	/product="thioredoxin h"	
	/protein_id="PAA04864.1"	
	/db_xref="GI:426442"	
	/translation="MAAEQGVVIACHKDEPDAOMTAKENGVYIIDFASKQPPR	
	FIATVEFAKKEPFAVLEKRVDELVEAKYVEMPTFLITKDAEDAKVGGARR	
	DDLONTIVKHNHGAFAASASA"	
BASE COUNT	171 a 150 c 182 g 184 t	
ORIGIN		
Alignment Scores:		
Pred. NO.:	2.92e-37	Length: 687
Score:	406.00	Matches: 75
Percent Similarity:	78.99%	Conservative: 19
Best local Similarity:	63.03%	Mismatches: 25
Query Match:	65.70%	Indels: 0
DB:	8	Gaps: 0
US-09-786-715-8 (1-123) x R1C7H (1-687)		
OY	5	GIUGLUGLGIYVAlIleGlyVAlIHISThrValAspGIUTRPLysLeuGlnLeuGlnAsn 24
Db	66	GAGGAGGAGTGCIGATCGCTGCCACCAACAGGAGGATTCGACGCCCAATGACCAAG 125
OY	25	AlAlAspSerIysLysLeuIleValValAspPheThrAlaSerTyrCysGlyProCys 44
Db	126	GCCAAAGAGGCGCCCAAGTGTGCTATTAATGACTTCACTGCTTCTGCTGTGGCCCTTCG 185
OY	45	ArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGluLeuIlePheLeu 64
Db	186	CGCTTCATCGCCCGAGTGTGCGCAATATACCCCAAAAAGTCCCTGGAGTGTCTTCCTG 245
OY	65	LysValAspValAspGluValArgProValAlaGluGluLysTyrSerIleGluAlaMetPro 84
Db	246	AAAGTTATGTTGATGAGCTGACGAGGAAGTGTCTGAAAAGTACATGTTCGAGGCAATGCCG 305
OY	85	ThrPheLeuPheLeuLysAspGlyGluIleValAspLysValValGlyAlaSerLysAsp 104
Db	306	ACCTTCTATTCATCAACGATGTCGTCGAGGCTACCAAGGTCTGTGGCCCGACGAGAT 365
OY	105	AspLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAlaAlaSerSerSer 123

Db 366 GACCTCAGAACACCATGTCGTAAGCAGCTGCGTCCACTGCTGATCTGCTTCC 422

RESULT 12

LOCUS NTRNA 698 bp mRNA linear PLN 15-FEB-1994

DEFINITION N.tabacum mRNA for thioredoxin.

ACCESSION X58527

VERSION X58527.1 GI:20046

KEYWORDS thioredoxin.

SOURCE Nicotiana tabacum (common tobacco)

ORGANISM Nicotiana tabacum

REFERENCE 1 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 698)

REFERENCE 2 Marty, I. and Meyer, Y.

1 Nucleotide sequence of a cDNA encoding a tobacco thioredoxin

LOCUS Plant Mol. Biol. 17 (1), 143-147 (1991)

MEDLINE 91329721

PUBMED 1868216

REFERENCE 2 (bases 1 to 698)

Brugidou, C., Marty, I., Chartier, Y. and Meyer, Y.

The Nicotiana tabacum genome encodes two cytoplasmic thioredoxin

genes which are differentially expressed

LOCUS Mol. Gen. Genet. 238 (1-2), 285-293 (1993)

MEDLINE 93241165

PUBMED 8479434

REFERENCE 3 (bases 1 to 698)

Meyer, Y.

Direct Submission

Submitted (14-FEB-1991) Y. Meyer, Laboratoire de Physiologie et

Biology, Moleculaire Vegetale, Universite av de Villeneuve, 66860

Perpignan, France

Gene product is probably cytoplasmic.

COMMENT

FEATURES

source

location/Qualifiers

1..698

/organism="Nicotiana tabacum"

/mol_type="mRNA"

/strain="white Burley"

/db_xref="taxon:4097"

/clone_lib="plasmid PT219"

/dev_stage="in vitro cells"

1..682

/evidence=experimental

79..459

/codon_start=1

/product="thioredoxin"

/protein_id="CAA1415.1"

/db_xref="GI:20047"

/db_xref="SWISS-PROT:P29449"

/translation="MAANDATSEGGVFGCHKVENNEYFKKGVETKKLVVDFTAS

WCGCRFIAPLADIARKMPHIVFLKVDVDELKTVSAEMSVEMPTFVFINDKEVDK

VGAKKEELOOTYIKHAAPIVTA"

468..473

polyA_signal

511..517

polyA_site

BASE COUNT 192 a 117 c 164 g 225 t

ORIGIN

Alignment Scores:

Pred. No.: 5.04e-37 Length: 698

Score: 404.00 Matches: 72

Percent Similarity: 83.78% Conservative: 21

Best Local Similarity: 64.86% Mismatches: 18

Query Match: 65.37% Indels: 0

DB: 8 Gaps: 0

US-09-786-715-8 (1-123) x NTRNA (1-698)

QY 5 GluGluGlyGlnValIleGlyValHisThrValaspGluTrpLysLeuGlnLeuGlnAsn 24

|||||

Db 106 GAGAGGAGACAAAGTTCGCTGCCACAGAGTTGAGGAATGGAACGAGTACTCTCAAGAA 165

QY 25 AlalysaspseryLysLeuIleValValaspPheThrAlaSerTrpCysGlyProCys 44

|||||

Db 166 GGCCTTAGACTAAGAACTGGTGGTCGATTTTACTGCTTATGCTGGGCCCTTGC 225

QY 45 ArgPheMetAlaProValLeuAlaGluIleAlaLysLysTrpProGluLeuIlePheLeu 64

|||||

Db 226 GCTTTATTCGCCCAATCTTCTGTCGACATTCCTAAGAAAGAGCCCAATATATTCCTC 285

QY 65 LysValaspValaspGluValArgProValAlaGluGluTrpLysLeuIleGluAlaMetPro 84

|||||

Db 286 AAGGTGATGTGATGAGAACTGATGACGCGGAGATGAGTGTGAGGCAATGGCA 345

QY 85 ThrPheLeuPheLeuLysaspGlyValIleValaspLysValValGlyAlaSerLysasp 104

|||||

Db 346 ACTTTTGTCTTCATTAAAGATGGAAGAAAGATGGACAGAGTTGTTGGCCAGAAAGAG 405

QY 105 AspleuGlnAlaThrIleAlaLysHisAlaSer 115

|||||

Db 406 GAGTTGCAGACACCATGATGTAAGCATCTGCT 438

RESULT 13

AF483265

LOCUS AF483265 345 bp mRNA linear PLN 01-APR-2002

DEFINITION Populus tremula x Populus tremuloides thioredoxin H mRNA, complete

ACCESSION AF483265

VERSION AF483265.1 GI:19851971

KEYWORDS cds.

ORGANISM Populus tremula x Populus tremuloides

Populus tremula x Populus tremuloides

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.

1 (bases 1 to 345)

REFERENCE 1 Behm, M. and Jacquot, J. P.

Isolation and characterization of thioredoxin h from poplar xylem

LOCUS Plant Physiol. Biochem. 38 (5), 363-369 (2000)

REFERENCE 2 Behm, M. and Jacquot, J. P.

Direct Submission

Submitted (13-FEB-2002) Faculte des Sciences, Universite Henri

Poincare, Bd des Aiguillettes, Vandoeuvre 54506, France

COMMENT

FEATURES

source

location/Qualifiers

1..345

/organism="Populus tremula x Populus tremuloides"

/mol_type="mRNA"

/db_xref="taxon:47664"

1..345

/codon_start=1

/product="thioredoxin H"

/protein_id="NAL9941.1"

/db_xref="GI:19851972"

/translation="MAEEGVYACHTVDYKREHREKSGSKLIVDFTASMPCKK

IAPFAPLAKKFPNVTFLKVDVDELKVAEBMVEAPPTFLFLDKRLVDTYGAADK

GLPTLVAKHATA"

BASE COUNT 101 a 61 c 95 g 88 t

ORIGIN

Alignment Scores:

Pred. No.: 4.78e-37 Length: 345

Score: 401.00 Matches: 73

Percent Similarity: 80.36% Conservative: 17

Best Local Similarity: 65.18% Mismatches: 22

Query Match: 64.89% Indels: 0

DB: 8 Gaps: 0

US-09-786-715-8 (1-123) x AF483265 (1-345)

QY 5 GluGluGlyGlnValIleGlyValHisThrValaspGluTrpLysLeuGlnLeuGlnAsn 24

|||||

Db 7 GAGAGGAGACAAAGTTCGCTGCCACAGAGTTGAGGAATGGAACGAGTACTCTCAAG 66

QY 25 AlalysaspseryLysLeuIleValValaspPheThrAlaSerTrpCysGlyProCys 44

```

Db      67 GGAAGAGCTCAGAACTGATGTCGTGATTTACTGCTCATGATGTCACCATGT 126
Oy      45 ArgpmetalaProvalleualagullalealyslysthrProgluleleleu 64
Db      127 AAATGATGTCACATCTTCCCGAGTGGGAGAAAGTTCACATGCAATCTTG 186
Oy      65 LysValaspValaspgluvalArgproValalagluglutysertleglulametro 84
Db      187 AAGGTGATGTGATGATGAATGAAGCTGTGCTGAGAGCTGGAATGTGAGGCAATGCCA 246
Oy      85 ThrleuPheleuleulysaspgluileuValaspLysValalgluLaserlyasp 104
Db      247 ACTTTATTTCTCTGGAAGATGCAAAATTAAGTGACAAACATGTGGCTCTGATTAAGAT 306
Oy      105 AspleuGlinalthrllealalysHsAlasera1a 116
Db      307 GGCCTGCCAACACTGTTGCCAAAGCACGCACTGCA 342

RESULT 14
TAE9762      596 bp      mRNA      linear      PLN 15-AUG-2001
LOCUS        Triticum aestivum mRNA for Chlorodoxin H.
ACCESSION   AJ009762.1 GI:4138593
VERSION     AJ009762.1 GI:4138593
KEYWORDS    Triticum aestivum (bread wheat)
SOURCE      Triticum aestivum
ORGANISM    Triticum aestivum
REFERENCE   1 Serrato,A.J., Crespo,J.L., Florencio,F.J. and Cejudo,F.J.
AUTHORS     Characterization of two thioresdoxins h with predominant
TITLE        localization in the nucleus of aleurone and scutellum cells of
JOURNAL      Plant Mol. Biol. 46 (3), 361-371 (2001)
MEDLINE     21380673
PUBMED      11488482
REFERENCE   2 (bases 1 to 596)
AUTHORS     Cejudo,F.J.
TITLE        Direct Submission
JOURNAL      Submitted (24-JUL-1998) Cejudo F.J., Instituto de Bioquímica
              Vegetal y Fotosíntesis, Universidad de Sevilla y CSIC, Avda Americo
              Vespucio s/n, 41092-Sevilla, SPAIN
FEATURES     source
              location/Qualifiers
              1..596
               /organism="Triticum aestivum"
               /mol_type="mRNA"
               /cultivar="Chinese Spring"
               /db_xref="taxon:4565"
              1..596
               /gene="thioresdoxin H"
              3'UTR
               /gene="thioresdoxin H"
               /gene="thioresdoxin H"
               /gene="thioresdoxin H"
polyA_signal
               /gene="thioresdoxin H"
BASE COUNT  161 a 127 c 182 g 126 t
ORIGIN
Alignment Scores:
Pred. No.:      2,64e-36      Length:      596
Score:          397.00      Matches:      68
Percent Similarity: 82.618      Conservative: 27
Best Local Similarity: 59.13%      Mismatches: 20
Query Match:    64.24%      Indels:      0
DB:            8      Gaps:      0

US-09-786-715-8 (1-123) x TAE9762 (1-596)
Oy      2 AlaguValaglulgluValalleglValalsthrValaspLutrylryLengln 21
Db      85 GCGGCGGTGGGGGGGGAGGTGATCTCCACACACCCCTGGAGAGTGCACATGCAG 144

```

```

Oy      22 LenglnAsnAlalysaspserLyslyleuileValaspPheThralasertrpCys 41
Db      145 ATCGAGAGAGCCACACCCGCCACAGAGCTGGGGGTTGACTTCATCTCATCATGTGT 204
Oy      42 GlyProCyArgPheMetAlaProvalleualagullalealyslysthrProgluleu 61
Db      205 GGACCATGGCGCATATGCTCCAGTTTCCGCTGATCTCGCCACAGAAATGCCAATGCT 264
Oy      62 llePheleuleulysaspgluvalArgproValalaglulgluLaserlyasp 81
Db      265 GTTTTCCTCAAGTCGATGTCATGATGAAGACCCATTCGAGCAATTCAGCGTTGAG 324
Oy      82 AlameProthPheleuPheleuleulysaspgluileuValaspLysValalgluL 101
Db      325 GCCATGCCAACCTCTCTGTCATTAAGAGAGAGATGTAAGAGAGGAGGTTGGAGCT 384
Oy      102 SerLysaspPheleuGlinalthrllealalysHsAlasera1a 116
Db      385 ATCAAGAGAGAACTGACGACAAAGTTGGGCTACACGCGGCGCC 429

RESULT 15
AY271308      784 bp      mRNA      linear      PLN 12-MAY-2003
LOCUS        Citrus x paradisi thioresdoxin H mRNA, complete cds.
ACCESSION   AY271308
VERSION     AY271308.1 GI:30575685
KEYWORDS    Citrus x paradisi
SOURCE      Citrus x paradisi
ORGANISM    Citrus x paradisi
REFERENCE   1 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE        rosids; eucosids II; Sapindales; Rutaceae; Citrus.
JOURNAL      1 (bases 1 to 784)
AUTHORS     Porat,R., Ben-Yephet,M. and Drobny,S.
TITLE        Isolation of a thioresdoxin H cDNA from grapefruit induced by yeast
              and fungal treatments
              unpublished
JOURNAL      2 (bases 1 to 784)
AUTHORS     Porat,R., Ben-Yephet,M. and Drobny,S.
TITLE        Direct Submission
JOURNAL      Submitted (08-APR-2003) Postharvest Science, ARO, The Volcani
              Center, Dorech Hamacabin, Bet Dagan 50250, Israel
FEATURES     source
              location/Qualifiers
              1..784
               /organism="Citrus x paradisi"
               /mol_type="mRNA"
               /db_xref="taxon:37656"
              190..561
               /codon_start=1
               /product="thioresdoxin H"
               /protein_id="AAP33009.1"
               /db_xref="GI:30575686"
               /translation="MAEEGVISCHTVESNMQLOKGIARKLIVDFPASCPCPKL
              MSPILSELAKLPVILFKVDYDELQSAVEEAAVEMPFVLTGKYLRLVAKKD
              ELQLAVERKATIVENATPRNA"
BASE COUNT  236 a 141 c 186 g 214 t 7 others
ORIGIN
Alignment Scores:
Pred. No.:      1,05e-35      Length:      784
Score:          393.00      Matches:      70
Percent Similarity: 80.678      Conservative: 26
Best Local Similarity: 58.82%      Mismatches: 23
Query Match:    63.59%      Indels:      0
DB:            8      Gaps:      0

US-09-786-715-8 (1-123) x AY271308 (1-784)
Oy      5 glugluglgluValalleglValalsthrValaspLutrylryLenglnLengln 24
Db      196 GAGGAGGAGCAAGTGTATGCTGCACACTGTGATCTCGAACAGACAGACGTCACAAAG 255

```

```

QY 25 AlalysAspSerLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCys 44
Db 256 GGCATTGCGGCAAGAACTGATAGTGATTTTACGGCTTCATGTGCCCCCATGC 315
QY 45 ArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGluLeuIlePheLeu 64
Db 316 AAGTTGATGTCCTCCAAATTGAGTGAAATGGCGAAGAGCTCCCGCTGTCATATTCTTG 375
QY 65 LysValAspValAspGluValArgProValAlaGluGluIleLysSerIleGluAlaMetPro 84
Db 376 AAGGTGATGTTGATGATTCAGTCCGCTCCGCTGAGGATGGCTGTGGAGCCATGCG 435
QY 85 ThrPheLeuPheLeuLysAspGlyGluIleValAspLysValValGlyAlaSerLysAsp 104
Db 436 ACCTTGTACTGACGAAAGAGCGCAAGTCTCTGAGAGGATTTGGGAGCGCAGAGAAAGAT 495
QY 105 AspleuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAlaAlaSerSerSer 123
Db 496 GAGCTGCAGCTGGCTGTGCAAAAGCACGCAACACTGTGGAATGCAACTACTGCT 552

```

Search completed: August 17, 2003, 21:41:58
 Job time : 1904.81 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 17:46:53 ; Search time 172.913 Seconds

(without alignments)
1920.219 Million cell updates/sec

Title: US-09-786-715-8

Perfect score: 618

Sequence: 1 MAEVEGQVIGVHTVDENKL.....DDLQATIAKASVAASS 123

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL-frame+pn.model -DEV-xlp
-Q/cgn2.1/USPTO.spool/US09786715/runat.11082003.150513.6025/app_query.fasta.1.1052
-DB=N.Geneseq.19Jun03 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonsum62 -TRANS=human40.cdi
-LIST=45 -DOCALL=GEN-200 -THR SCORE=100 -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09786715.ecgn.1.1.874.0/runat.11082003.150513.6025 -NCP=6 -ICPU=3
-NO_MAP -LAKEOUTERY -NEG-SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N.Geneseq.19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	618	100.0	601	21	AAZ51740	Glycine max thior
2	565	91.4	390	25	ABX19403	Human GDP-mannose
3	515	83.3	392	25	ABX18045	Human GDP-mannose
4	446	72.2	574	21	AAZ51738	Catalpa speciosa t
5	425	68.8	402	25	ABX21664	Human GDP-mannose
6	418	67.6	738	21	AAZ51739	Glycine max thior
7	413	66.8	270	25	ABX31386	Human GDP-mannose
8	411	66.5	3888	24	ABX53097	DNA encoding Thior
9	411	66.5	3888	24	ABN89581	Phaseolin promoter
10	411	66.5	4935	24	ABN89586	Promoter-Oleosin t
11	410	66.3	345	24	AB212358	Arabidopsis thalia
12	410	66.3	345	24	ABN89587	Arabidopsis thalia
13	410	66.3	470	21	AAZ51781	Arabidopsis thalia
14	410	66.3	561	21	AAZ51522	Arabidopsis thalia
15	410	66.3	563	21	AAZ51741	Arabidopsis thalia
16	410	66.3	3129	24	ABX53095	DNA encoding thior
17	410	66.3	3129	24	ABN89579	Phaseolin promoter
18	410	66.3	3888	24	ABX89580	DNA encoding Oleos
19	410	66.3	3888	24	ABN89580	Phaseolin promoter
20	406	65.7	686	15	AAZ78205	Gene coding for pr
21	406	65.7	687	21	AAZ66375	Rice thiorodoxin h
22	404.5	65.5	509	22	AAH87768	Peppermint plant o
23	404	65.4	614	21	AAZ51741	Vernonia mespilifo
24	392	63.4	393	17	AAZ10451	Hard wheat thior
25	392	63.4	393	21	AAZ62457	Wheat thiorodoxin
26	392	63.4	653	16	AAZ09783	Plant SAR gene pl.
27	392	63.4	653	20	AAV62799	Tobacco SAR CHX in
28	392	63.4	653	20	AAV81683	Tobacco protein-sy
29	389	62.9	369	21	AAZ61537	Nucleotide sequenc
30	388	62.8	382	21	AAZ62456	Wheat thiorodoxin
31	388	62.8	384	17	AAZ10450	Soft wheat thior
32	387	62.6	419	21	AAZ31942	Plant microsatelli
33	380.5	61.6	360	24	ABZ12359	Arabidopsis thalia
34	376	60.8	370	21	AAZ62455	Barley thiorodoxin
35	376	60.8	560	21	AAZ41961	Arabidopsis thalia
36	374.5	60.6	590	21	AAZ38792	Arabidopsis thalia
37	374	60.5	357	24	AAZ13931	Arabidopsis thalia
38	374	60.5	480	21	AAZ36542	Arabidopsis thalia
39	374	60.5	563	21	AAZ34211	Arabidopsis thalia
40	374	60.5	652	21	AAZ48656	Arabidopsis thalia
41	373	60.4	524	21	AAZ33829	Arabidopsis thalia
42	367	59.4	576	25	ABX56868	Arabidopsis thalia
43	364	58.9	260	25	ABX30882	Human GDP-mannose
44	361	58.4	267	25	ABX31078	Human GDP-mannose
45	360	58.3	353	21	AAZ31118	Plant microsatelli

ALIGNMENTS

RESULT 1	AAZ51740	standard; cDNA: 601 BP.
ID	AAZ51740	
AC	AAZ51740	
XX		
DT	04-JUL-2000	(first entry)
XX		
DE	Glycine max thiorodoxin	CDNA-2.
XX		
KW	Glycine max thiorodoxin; clone sfil.pK0029.e2; chimeric gene; soybean;	
KM	transgenic Plant; seed storage protein; allergenicity; ss.	
XX		
OS	Glycine max.	
XX		
FT	Key	Location/Qualifiers
CDS		37..408

FT /*tag_ a
XX /product= "Thioredoxin"
XX
XX MO200014239-A2.
XX
XX 16-MAR-2000.
XX
XX 07-SEP-1999; 99WO-US20420.
XX
XX 08-SEP-1998; 98US-0099501.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Allen SM, Thorpe CJ, Lu AL;
XX
XX WPI: 2000-256987/22.
XX
XX P-PSDB: NAY70482.
XX
XX New isolated polynucleotide encoding thioredoxin polypeptide is useful
XX for producing transgenic plants with an altered level of thioredoxin -
XX
XX Claim 3; Page 30-31; 33pp; English.
XX
XX The present cDNA sequence encodes Glycine max thioredoxin protein. The
XX cDNA was derived from clone sfl1.pk0029.e2, which was isolated from a
XX cDNA library prepared from soybean immature flower. Chimeric genes
XX encoding all or a portion of the thioredoxin protein, in sense or
XX antisense orientation are constructed, wherein expression of the chimeric
XX gene results in production of altered levels of the thioredoxin protein
XX in a transformed host cell. Thioredoxin is involved in the disassembly of
XX seed storage proteins during germination by reducing S-S bonds and in the
XX bread making process. Over expression of thioredoxin in cereals may
XX reduce the allergenicity of any transgenic protein engineered into
XX cereal crops with high sulfhydryl content.
XX
XX Sequence 601 BP; 194 A; 103 C; 136 G; 168 T; 0 other;

Alignment Scores:
Pred. No.: 4,01e-74 Length: 601
Score: 618.00 Matches: 123
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-786-715-8 (1-123) x AA251740 (1-601)

QY 1 Metlaagluvalgiugluylglnvallellyvalhsthrvalaspclutrpplysleu 20
DB 37 ATGGCTGAAGTGAAGAGGACAGTGTATCGCGCTCCACACCGTGTGATGAGTGAAGCTG 96
QY 21 Glnleuglnasnalaalsaspserslylsleullevalvalaspheerthralasertrp 40
DB 97 CAACTCCAGAAATGAAGAAAGCTCCAAAGAACTGATGGGGGATTTTACGCTTCCGG 156
QY 41 Cysgliprocysatrgpmetalaiprovalleualagluilealalyslysthrproglu 60
DB 157 TGTGCTCATGCGCTTTTATGGCCCAAGTCTTCCAGAGATTGCAAGAAACCCCTGAA 216
QY 61 Leuilepheleulysvalaspvalaspcluvallargprovalalaglulutyrsertle 80
DB 217 TTGATCTTCCCTCAAGATGATGATGATGAGCTGCTGTGCTGAGAGATATTCATTT 276
QY 81 Glualametprothrphelheulysaspclylulilevalaspplysvalvalgly 100
DB 277 GAGGCATGCCAACCTTCTCTCTTGAAGATGGCGAGATCGGCAAGGTGGTGGT 336
QY 101 Alaserlyaspaapleuglnalathrillealalyslyshisalaseralalvalalala 120
DB 337 GCTTGTAAGATGACCTTCAAGCCACCATAGCAAGCATGATGCTGCTGCTGCT 396
QY 121 Serserser 123
|||||||

DB 397 TCTTCTTCT 405

RESULT 2

ABX19403

ID ABX19403 standard; cDNA; 390 BP.

AC ABX19403;

DT 10-FEB-2003 (first entry)

XX Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #1460.

XX Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;
XX cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
XX arthritis; asthma; sepsis; reperfusion injury; stroke; infection;
XX complex carbohydrate; gene replacement therapy; immunosuppressive;
XX antiinflammatory; antirheumatic; antibacterial; cerebroprotective;
XX antiasthmatic; vasotropic.

OS Homo sapiens.

XX US2002110548-A1.

XX 15-AUG-2002.

XX 11-JUN-2001; 2001US-0878574.

XX 22-NOV-1996; 96US-0753233.

XX 03-DEC-1997; 97US-0984246.

XX 09-SEP-1998; 98US-0149674.

XX 14-JUN-1999; 99US-0333177.

XX (GEMY) GENETICS INST INC.

XX Sullivan F, Kriz R, Kumar R;

XX WPI: 2003-066673/06.

XX New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
XX peptide, for manufacturing complex carbohydrates, or as targets for
XX screening GM4,6D antagonists for treating e.g. arthritis, or transplant
XX rejection -
XX
XX Disclosure: SEQ ID NO 1462; 6pp; English.

XX The invention relates to a composition comprising a human GDP-mannose
XX 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
XX GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation
XX in a mammalian subject and for treating or ameliorating diseases affected
XX by the level of cellular fucosylation or diseases affected by the
XX fucosylation of glycoconjugates. These diseases include arthritis,
XX transplant rejection, asthma, sepsis, reperfusion injury, stroke or
XX infection. The GM4,6D peptide or a polynucleotide encoding it is also
XX useful for manufacturing complex carbohydrates and as targets for
XX screening small molecule antagonists of the activity of the enzyme. The
XX polynucleotide is useful in developing an assay for defects in the
XX enzyme, as well as in gene replacement therapy. Sequences
XX ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding
XX human GM4,6D peptides of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format directly from USPTO
XX at seqdata.uspto.gov/sequence.html.

XX Sequence 390 BP; 97 A; 86 C; 97 G; 110 T; 0 other;

Alignment Scores:

Pred. No.: 3.35e-67 Length: 390
Score: 565.00 Matches: 111
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 91.42% Indels: 0
DB: 25 Gaps: 0

US-09-786-715-8 (1-123) x ABX19403 (1-390)

QY 1 MetAlaGluValGluGluGluValIleGlyValHisThrValAspGluTrpLysLeu 20
DB 57 ATGGCTGAAGTGAAGACAGACAGTCATCGGCTCACACCTGATGATGAGGAGCTG 116
QY 21 GlnLeuGlnAsnAlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTTP 40
DB 117 CAACCTCCAGATGCCAAGACTCCAAAAAATCATGTTGTGTGATTTTACTGCTTCTG 176
QY 41 CysGlyProCysArgPheMetAlaProValIleuAlaGluIleAlaLysIsthrProGlu 60
DB 177 TGGGTGCATGCGCTTTATGCGCCAGTTCTGCAGAGATTCCAAGAAACTCTCGAA 236
QY 61 LeuIlePheLeuLysValAspValAspGluValArgProValAlaGluGluTrpSerTle 80
DB 237 TTGATCTTCCTCAAACTGATGATGAGTGAAGTGAAGCTGTGCTAGAGAAATTCCTCAAT 296
QY 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyGluIleValAspLysValAlaGly 100
DB 297 GAGGCCATGCCAACCTTCTCTTCTTGAAGAATGCGGCAATCGTGACAAAGTGTGGT 356
QY 101 AlaSerLysAspAspLeuGlnAlaThrIleAla 111
DB 357 GCTAGTAAGATGACCTTCACAGCCACCATAGCC 389

RESULT 3
ABX18045
ID ABX18045 standard; cDNA; 392 BP.

AC ABX18045;
XX
DT 10-FEB-2003 (first entry)

DE Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #102.
XX
XX Human: GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;
KW cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
KW arthritis; asthma; sepsis; reperfusion injury; stroke; infection;
KW complex carbohydrate; gene replacement therapy; immunosuppressive;
KW antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
KW antidiabetic; vasotropic.

OS Homo sapiens.
XX
PN US2002110548-A1.
XX
PD 15-AUG-2002.
XX
PF 11-JUN-2001; 2001US-0878574.
XX
PR 22-NOV-1996; 96US-0753233.
PR 03-DEC-1997; 97US-0984246.
PR 09-SEP-1998; 98US-0149674.
PR 14-JUN-1999; 99US-0333177.
XX
PA (GENW) GENETICS INST INC.
XX
PI Sullivan F, Kriz R, Kumar R;
XX
XX WPI; 2003-066673/06.
XX
PT New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
PT peptide, for manufacturing complex carbohydrates, or as targets for
PT screening GM4,6D antagonists for treating e.g. arthritis, or transplant
PT rejection
XX
PS Disclosure: SEQ ID NO 104; 6pp; English.
XX
CC The invention relates to a composition comprising a human GDP-mannose
CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
CC GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation
CC in a mammalian subject and for treating or ameliorating diseases affected

CC by the level of cellular fucosylation or diseases affected by the
CC fucosylation of glycoconjugates. These diseases include arthritis,
CC transplant rejection, asthma, sepsis, reperfusion injury, stroke or
CC infection. The GM4,6D peptide or a polynucleotide encoding it is also
CC useful for manufacturing complex carbohydrates and as targets for
CC screening small molecule antagonists of the activity of the enzyme. The
CC polynucleotide is useful in developing an assay for defects in the
CC enzyme, as well as in gene replacement therapy. Sequences
CC ABX1942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding
CC human GM4,6D peptides of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html.
XX

SEQ Sequence 392 BP; 99 A; 80 C; 107 G; 106 T; 0 other;

Alignment Scores:
Pred. No.: 2,02e-60 Length: 392
Score: 515.00 Matches: 98
Percent Similarity: 92.31% Conservative: 10
Best Local Similarity: 83.76% Mismatches: 9
Query Match: 83.33% Indels: 0
DB: Gaps: 0

US-09-786-715-8 (1-123) x ABX18045 (1-392)

QY 5 GluGluGlyGlnValIleGlyValHisThrValAspGluTrpLysLeuGlnAsn 24
DB 12 GAAAGAGGTGACAGTGTGCGCGTCCACACCGTGTGATGCGTGAACGACAGTGCAGAAAT 71
QY 25 AlaLysAspSerLysLysLeuIleValAspPheThrAlaSerTrpCysGlyProCys 44
DB 72 GCAAAAGACTCCCAAAATTTGATTGTGGGATTTACTGCTTCTGGTGTGATCCATGC 131
QY 45 ArgPheMetAlaProValIleuAlaGluIleAlaLysIsthrProGluLeuIlePheLeu 64
DB 132 CGTTTATATGCCCACTGCTGCGAGAGATGCTAGCAGAACATCCCAAGATCTTCC 191
QY 65 LysValAspValAspGluValArgProValAlaGluGluTrpSerIleGluAlaMetPro 84
DB 192 AAGGTGATGTGATGATGAGTGAAGCTGTGCTGAGGAATATTCCTAGGCGCATGCCA 251
QY 85 ThrPheLeuPheLeuLysAspGlyGluIleValAspLysValAlaGluLysAsp 104
DB 252 ACCTTCCTCTCTTGAAGATGCGACAGATCGTGAATAGCTGTGTGCTAAGAAAGAG 311
QY 105 AspLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAlaLaser 121
DB 312 GAGCTCACACTCACCATAGCCAAAGCATGTATCTGCTGCTGCTTCTCT 362

RESULT 4
AAZ51738
ID AAZ51738 standard; cDNA; 574 BP.
XX
XX AAZ51738;
XX
DT 04-JUL-2000 (first entry)
XX
DE Catalpa speciosa thiorodoxin cDNA.
XX
XX Catalpa speciosa thiorodoxin; clone ncs.pk0010.e3; chimeric gene;
KW transgenic plant; seed storage protein; allergenicity; ss.
XX
OS Catalpa speciosa.
XX
XX
XX Key Location/Qualifiers
XX FT 63..419 /tag= a
XX FT /product= "thiorodoxin"
XX
PN WO200014239-A2.
XX
PD 16-MAR-2000.

XX 07-SEP-1999; 99WO-US20420.
PF 08-SEP-1998; 98US-0099501.
PR
XX (DUPO) DU PONT DE NEMOURS & CO E. I.
PA
PI Allen SM, Thorpe CJ, Lu AL;
XX WPI: 2000-256987/22.
DR P-PSDB: AAY70480.
XX
XX New isolated polynucleotide encoding thioredoxin polypeptide is useful
PT for producing transgenic plants with an altered level of thioredoxin -
XX
XX Claim 3; Page 29; 33pp; English.
XX
XX The present CDNA sequence encodes Catalpa speciosa thioredoxin
CC protein. The CDNA was derived from clone ncs.pk0010.63, which was
CC isolated from a CDNA library prepared from C. speciosa developing seed
CC tissue. Chimeric genes encoding all or a portion of the thioredoxin
CC protein, in sense or antisense orientation are constructed, wherein
CC expression of the chimeric gene results in production of altered levels
CC of the thioredoxin protein in a transformed host cell. Thioredoxin is
CC involved in the disassembly of seed storage proteins during germination
CC by reducing S-S bonds and in the bread making process. Over expression of
CC thioredoxin in cereals may reduce the allergenicity of any transgenic
CC protein engineered into cereal crops with high sulfhydryl content.
XX
XX Sequence 574 BP; 171 A; 91 C; 157 G; 155 T; 0 other;
SO
Alignment Scores:
Pred. No.: 7.76e-51 Length: 574
Score: 446.00 Matches: 80
Percent Similarity: 85.59% Conservative: 21
Best Local Similarity: 67.80% Mismatches: 17
Query Match: 72.17% Indels: 0
DB: Gaps: 0
US-09-786-715-8 (1-123) x AA251738 (1-574)
QY 1 MetAlaGluValAlaGluGluGluValAlaHisThrValAspGluTrpLysLeu 20
DB 63 ATGGCTCTTCAGAAAGGAGGCAAGTGCCTGCCACCTCCGACGACTGGAAGCAG 122
QY 21 GlnLeuGlnAsnAlaLysAspSerLysLeuIleValValAspPheThrAlaSerTrp 40
DB 123 CAGTTCAGAAAGGCTGTGACTCTAAGAAACTGGTGGTAATAGACTTCACGGCTTCCG 182
QY 41 CysGlyProCysArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGlu 60
DB 183 TGCAGCAGCAGCCCTTCATGCTCAATCTTGGCTGAGAGGCCAAGAACACCCCAT 242
QY 61 LeuIlePheLeuLysValAspValAspGluValArgProValAlaGluTrpSerIle 80
DB 243 GTCAATATTCCTGAAGAGTGCAGCTGATGAAGCTGAGTGTGAGAAATTCAAAGTG 302
QY 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyGluIleValAlaAspLysValAlaGly 100
DB 303 GAGGCTAATGCCGACCTTCGTCTCCCAAGGAAGGAAGGAAGGAAGGCTTGTGGA 362
QY 101 AlaSerLysAspAspLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAla 118
DB 363 GCAAGGAAGGAGAAATTCAGCCACAGTGTGAGAAACATGCGCTATCATCGCT 416
RESULT 5
ABX21664
ID ABX21664 standard; CDNA: 402 BP.
XX
AC ABX21664;
XX
DT 10-FEB-2003 (first entry)
XX

DE Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #3721.
XX
XX Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;
KW cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
KW arthritis; asthma; sepsis; reperfusion injury; stroke; infection;
KW complex carbohydrate; gene replacement therapy; immunosuppressive;
KW antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
KW antiasthmatic; vasotropic.
XX
XX Homo sapiens.
XX
XX US2002110548-A1.
XX
XX 15-AUG-2002.
XX
XX 11-JUN-2001; 2001US-0878574.
XX
XX 22-NOV-1996; 96US-0753233.
XX 03-DEC-1997; 97US-0984246.
XX 09-SEP-1998; 98US-0149674.
XX 14-JUN-1999; 99US-0333177.
XX
XX (GENV) GENETICS INST INC.
XX
XX Sulliyvan F, Kriz R, Kumar R;
XX
XX WPI: 2003-066673/06.
XX
XX New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
PT peptide, for manufacturing complex carbohydrates, or as targets for
PT screening GM4,6D antagonists for treating e.g. arthritis, or transplant
PT rejection
XX
XX Disclosure; SEQ ID NO 3723; 6pp; English.
XX
XX The invention relates to a composition comprising a human GDP-mannose
CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
CC GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation
CC in a mammalian subject and for treating or ameliorating diseases affected
CC by the level of cellular fucosylation or diseases affected by the
CC fucosylation of glycoconjugates. These diseases include arthritis,
CC transplant rejection, asthma, sepsis, reperfusion injury, stroke or
CC infection. The GM4,6D peptide or a polynucleotide encoding it is also
CC useful for manufacturing complex carbohydrates and as targets for
CC screening small molecule antagonists of the activity of the enzyme. The
CC polynucleotide is useful in developing an assay for defects in the
CC enzyme, as well as in gene replacement therapy. Sequences
CC ABX17942-ABX17944 and ABX17947-ABX3716 represent DNA molecules encoding
CC human GM4,6D peptides of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 402 BP; 113 A; 76 C; 122 G; 91 T; 0 other;
SO
Alignment Scores:
Pred. No.: 3.31e-48 Length: 402
Score: 425.00 Matches: 77
Percent Similarity: 86.49% Conservative: 19
Best Local Similarity: 69.37% Mismatches: 15
Query Match: 68.77% Indels: 0
DB: Gaps: 0
US-09-786-715-8 (1-123) x ABX21664 (1-402)
QY 5 GluGluGlyGluValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsn 24
DB 49 GAAGAGGAGCAAGTGCAGTGGTCTCACAGCCTTACAGGAGTGAAGAACATCTCAAGAG 108
QY 25 AlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCys 44
DB 109 GGAAGAGAGTCCAGAAATTCATGCTGTGATTTTACTGCTTGTGCGGTCATGCC 168

XX The invention relates to a composition comprising a human GDP-mannose
CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
CC GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation
CC in a mammalian subject and for treating or ameliorating diseases affected
CC by the level of cellular fucosylation or diseases affected by the
CC fucosylation of glycoconjugates. These diseases include arthritis,
CC transplant rejection, asthma, sepsis, reperfusion injury, stroke or
CC infection. The GM4,6D peptide or a polynucleotide encoding it is also
CC useful for manufacturing complex carbohydrates and as targets for
CC screening small molecule antagonists of the activity of the enzyme. The
CC polynucleotide is useful in developing an assay for defects in the
CC enzyme, as well as in gene replacement therapy. Sequences
CC ABX17942-ABX17944 and ABX17947-ABX3716 represent DNA molecules encoding
CC human GM4,6D peptides of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html.

XX Sequence 270 BP; 69 A; 53 C; 71 G; 77 T; 0 other;

Alignment Scores:

Pred. No.: 8,03e-47 Length: 270
Score: 413.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.83% Indels: 0
DB: 25 Gaps: 0

US-09-786-715-8 (1-123) x ABX31386 (1-270)

QY 1 MetAlaGluValAlGluGluGluValAlIleGlyValAlHisThrValAlAspGluTrpLysLeu 20
DB 29 ATGGCTGAAGTGAAGAGGAGGAGGTATCGCGCCACACCGTTGATGAGTGAAGCTG 88
QY 21 GluLeuGlnAsnAlaLysAspSerLysLysLeuIleValAlAspPheThrAlaSerTrp 40
DB 89 CAACTCCAGATGCAAAAGACTCCAAAAACTGATTTGGTGGATTTTACTGCTCCCTGG 148
QY 41 CysGlyProCysATGpPheMetAlaProValLeuAlaGluIleAlaLysLysTrpProGlu 60
DB 149 TGTGCTCATGCTCCGTTTATGCCCCAGCTTCTTGCAAGATTGCCAAGAAACCTCTGAA 208
QY 61 LeuIlePheLeuLysValAlAspValAlAspGluValAlArgProValAlaGluGluTrpSerIle 80
DB 209 TTGATCTTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 268

RESULT 8

ABSS3097
ID ABSS3097 standard; DNA; 3888 BP.

XX AC ABSS3097;

DT 29-NOV-2002 (first entry)

XX DNA encoding Thioiredoxin-oleosin fusion protein.

KW Thioiredoxin; thioiredoxin reductase; gene expression; oleosin;
KW oil body; oleosin-thioiredoxin fusion protein; gene; ds.

XX Arabidopsis thaliana.

OS Brassica napus.

OS Synthetic.

XX Key location/Qualifiers

FT CDS 1555..2658
FT /tag= a
FT /product= "Thioiredoxin-oleosin fusion protein"

FT exon 1555..2250
FT /tag= b
FT /number= 1

FT Intron 2251..2489
FT /tag= c

FT /number= 1
FT exon 2490..2658
FT /tag= d
FT /number= 2

US2002088025-A1.

04-JUL-2002.

03-JUL-2001; 2001US-0897425.

22-FEB-1991; 91US-0659835.

16-NOV-1993; 93US-0142418.

30-DEC-1994; 94US-0366783.

25-APR-1997; 97US-0846021.

18-DEC-1998; 98US-0210843.

(MOLO/) MOLONEY M. M.
(DALM/) DALMIA B. K.

MoJoney NM, Dalmlia BK;

WPI: 2002-635723/68.

Expressing protein, by introducing chimeric nucleotide regulatory
sequence, sequence encoding fusion protein, having sequence encoding
protein, oleosin gene and sequence encoding termination region and
producing protein

Example 21; Fig 14; 69pp; English.

XX The invention describes a method of expressing thioiredoxin or thioiredoxin
CC reductase (I) in the oil body of a host cell using an oil body protein
CC gene. The method involves introducing a chimeric nucleic acid comprising
CC a first sequence to regulate transcription, a second DNA sequence
CC encoding a fusion polypeptide, comprising a sequence encoding an oleosin
CC gene and sequence encoding (I) and a third sequence encoding a
CC termination region functional in the host cell and growing the host cell
CC to produce a fusion polypeptide. The method or (I) is useful for
CC expression of a thioiredoxin or thioiredoxin reductase by a host cell. This
CC sequence encodes a thioiredoxin oil body protein fused to Arabidopsis thaliana
CC thioiredoxin gene controlled by a phaseolin promoter and phaseolin
CC terminator sequence.

SQ Sequence 3888 BP; 1254 A; 722 C; 613 G; 1299 T; 0 other;

Alignment Scores:

Pred. No.: 6,26e-45 Length: 3888
Score: 411.00 Matches: 74
Percent Similarity: 81.90% Conservative: 21
Best Local Similarity: 63.79% Mismatches: 21
Query Match: 66.50% Indels: 0
DB: 24 Gaps: 0

US-09-786-715-8 (1-123) x ABSS3097 (1-3888)

QY 5 GluGluGluGluValAlIleGlyValAlHisThrValAlAspGluTrpLysLeuGlnLeuGlnAsn 24

DB 1564 GAAGAAGACAGCAAGATGCGCTGCCACACCGTTGAGACATGAGACAGACACTTCAGAG 1623

QY 25 AlaLysAspSerLysLysLeuIleValAlAspPheThrAlaSerTrpCysGlyProCys 44

DB 1624 GCTAATGATCAAAAGCTGTTGATGATTTCAAGCGCTCTGTTGTTGGTGGACCATGT 1683

QY 45 ArgPheMetAlaProValLeuAlaGluIleAlaLysLysTrpProGluLeuIlePheLeu 64

DB 1684 CGTTTCATCGCTCAATCTTGTGATTTGGCTAAGAACTTCCTAAGTCTTTCCTC 1743

QY 65 LysValAlAspValAlAspGluValAlArgProValAlaGluGluTrpSerIleGluAlaMetPro 84

DB 1744 AAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1803

QY 85 ThrPheLeuPheLeuLysAspGlyGluIleValAlAspLysValAlGlyAlaSerLysAsp 104

Db 1804 ACCTTCATGTTTTCGAAGAGGAGACATTTTGGACAAAGTTGTTGGAGCCCAAGAACAT 1863
105 AspleuglnaIarhrrlealalyHisAlaSerAlaValAlaAla 120
:::|||||:::
1864 GAGCTTCAGTCTACCATTTGCCAACAACCTTGCTATGGCGATACAGCT 1911

RESULT 9
ABN89581
ID ABN89581 standard; DNA: 3888 BP.
XX
AC ABN89581;
XX
DT 06-SEP-2002 (first entry)
XX
DE Phaseolin promoter-Trxh oleosin-phaseolin terminator DNA SEQ:19.
XX
KW Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
KW oil body; ophthalmological; antidiabetic; cytosolic; antiprolifer;
KW vasotrophic; vulnerrary; antibacterial; immunosuppressive; antiulcer;
KW food product; milk; wheat; oxidative stress; cataract; diabetes;
KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KW bronchiolpulmonary disease; malignancy; reperfusion injury; wound healing;
KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
KW gastro oesophageal reflux disease; gene; ds.
XX
XX Arabidopsis sp.
OS Phaseolus vulgaris.
XX
XX Phaseolus vulgaris.
XX
XX MO200250289-A1.
PN
PD 27-JUN-2002.
XX
XX 19-DEC-2001; 2001WO-US50240.
PR
XX 19-DEC-2000; 2000US-0742900.
PR 05-JUL-2001; 2001US-302885P.
PR 04-DEC-2001; 2001US-0006038.
XX
XX (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmlia BK;
PI Del Val G, Zaplachinski S, Moloney M;
XX
XX WPI: 2002-508806/54.
DR P-PSDB; ABP60683.
XX
XX Example 2: Page 169-171; 362pp; English.
XX
XX The present invention describes a method (M1) for producing an oil body
XX associated with a recombinant multimeric protein complex (MPC). M1
XX comprises producing in a cell comprising oil bodies a first and second
XX recombinant polypeptide (P1, P2), where P1 is capable of associating
XX with P2 to form the MPC and associating the complex with an occlusion
XX body (OB) through an OB-targeting-protein capable of associating with OB
XX and P1. M1 is useful for producing an oil body associated with a
XX recombinant MPC. The oil bodies are further formulated for use in the
XX preparation of a food product such as milk or wheat based food product,
XX personal care product which reduces the oxidative stress on the surface
XX area of the human body or used to lighten the skin, or a pharmaceutical
XX composition used to treat chronic obstructive pulmonary disease (COPD),
XX cataracts, diabetes, envenomation, bronchiolpulmonary disease, psoriasis,
XX malignancies, reperfusion injury, wound healing, sepsis, gastro
XX intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
XX (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677
XX to ABP60964 represent sequence given in the exemplification of the
XX present invention.

XX	Sequence	3888 BP; 1254 A; 722 C; 613 G; 1299 T; 0 other;
SO	Alignment Scores:	
XX	Pred. No.:	6.26e-45 Length: 3888
XX	Score:	411.00 Matches: 74
XX	Percent Similarity:	81.90% Conservative: 21
XX	Best Local Similarity:	63.79% Mismatches: 21
XX	Query Match:	66.50% Indels: 0
XX	DB:	Gaps: 0
XX	US-09-786-715-8 (1-123) x ABN89581 (1-3888)	
QY	5 GluGluGluGluValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsn 24	
Db	1564 GAAAGAGGACAAAGTGAATGCGCTGCGCACACCGTGGAGACATGGAACGACACTTCAGAAAG 16233	
QY	25 AlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCys 44	
Db	1624 GCTAATGATCCAAACCTCTTGCGTGGTGAATTCACAGCGCTCTTGGTGGAGACAAAGT 16633	
QY	45 ArgPheMetAlaProValLeuAlaGluIleAlaLysLysTrpProGluLeuIlePheLeu 64	
Db	1684 CGTTTCATACGCTCATTTCTTTCGTCGATTTGGCTTAAGAACTTCTCAAGCTGCTTTTCTC 17433	
QY	65 LysValAspValAspGluValArgProValAlaGluGluLysTrpSerIleGluAlaMetPro 84	
Db	1744 AAGGTGTACTGATGATGATTAAGTGGGTGCGAAGTGAATGTCGCGATACAGCGATGCGCA 18033	
QY	85 ThrPheLeuPheLeuLysAspGlyGluIleValAspLysValValGlyAlaSerLysAsp 104	
Db	1804 ACCTTTCATGTTTGAAGGAGGAGATTTTGGACAAAGTTGTTGGAGCCAGAAAGAT 18633	
QY	105 AspLeuGlnAlaTrpIleAlaLysHisAlaSerAlaValAlaAlaIleAla 120	
Db	1864 GAGCTTCACTACCATTTGCCAAACACTTGGCTATGGCGGATACAGCT 1911	
XX	RESULT 10	
XX	ABN89586	
XX	ID ABN89586 standard; DNA; 4935 BP.	
XX	ABN89586;	
XX	06-SEP-2002 (first entry)	
XX	Promoter-Oleoin thiooredoxin reductase-linker-thiooredoxin-terminator #33.	
XX	Multimeric protein; redox protein; thiooredoxin; thiooredoxin reductase;	
XX	oil body; ophthalmological; antiabiotic; cytosolic; antiporter;	
XX	vasotrophic; vulnerary; antibacterial; immunosuppressive; antiulcer;	
XX	food product; milk; wheat; oxidative stress; cataract; diabetes;	
XX	chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;	
XX	bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;	
XX	gastro intestinal bleeding; intestinal bowel disease; ulcer;	
XX	gastro oesophageal reflux disease; gene; ds.	
XX	Arabidopsis sp.	
OS	Phaseolus vulgaris.	
XX	MO200250289-A1.	
XX	27-JUN-2002.	
XX	19-DEC-2001; 2001WO-US50240.	
XX	19-DEC-2000; 2000US-0742900.	
XX	05-JUL-2001; 2001US-30285P.	
XX	04-DEC-2001; 2001US-0006038.	
XX	(SEMB-) SEMBIOSYS GENETICS INC.	
XX	(SYGN) SYNGENTA PARTICIPATIONS AG.	
XX	Van Rooijen G., Deckers H., Helfetz PB., Briggs SP., Dalmia BK.	

PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132853.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134376.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0138119.
PR 16-JUN-1999; 99US-0138452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140623.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148177.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149126.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 23-AUG-1999; 99US-0150566.
PR 25-AUG-1999; 99US-0150584.
PR 26-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151348.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.

PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160880.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:

Pred. No.: 4,45e-46 Length: 470
Score: 410.00 Matches: 73
Percent Similarity: 85.32% Conservative: 20
Best Local Similarity: 66.97% Mismatches: 16
Query Match: 66.34% Indels: 0
DB: 21 Gaps: 0

US-09-786-715-8 (1-123) x AAC37781 (1-470)

QY 5 GIUGIUGIYGLNValIIleGIYValIHStrValAspGIUTrPlyslengInleugInasn 24
DB 104 GAGAGAGGACAGTAGTCCCTGCCACCGTTGAGACATGAGACAGAGCAGCTTCAGAG 163
QY 25 AlalysAspSerLysLysLeuIIleValValAspPheThrAlaSerTrpCysGlyProCys 44
DB 164 GCTATATGATCAAAACCTTGTGGGTGATTTTCACGGCTTCTTGGTGTGACCATAT 223
QY 45 ArgPheMetAlaProValIleuValaGIUleAlaLysLysThrProGIUleuIIlePheLeu 64
DB 224 CCTTCATCGCTCCATCTTCTTCTGCTGATTTGGCTAGAAACCTTCCTAACGCTTTTCCCTC 283
QY 65 LysValAspValAspGIUValArpProValAlaGIUTrpSerIIleGIUAlaMetPro 84
DB 284 AAGGTTGATACGTGATGAATTTGAAGTCGTGGCAAGTATGGCGGTACAGCGATGCCA 343
QY 85 ThrPheLeuPheLeuLysAspGIUleValIleValAspLysValValGIUValSerLysAsp 104
DB 344 ACCCTCATCTTTTTCAGAGAGGAGGAAGATTGTGGACAAAGTTGTGGAGCCAGAAAGAT 403
QY 105 AspLeuGIUAlaThrIIleAlaLysHls 113
DB 404 GAGCTTCAGCTACCATTCGCCAAACAC 430

RESULT 14

AAC51522
ID AAC51522 standard; DNA; 561 BP.

AAC51522;

18-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 68832.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

XX metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.
PD 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129645.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134321.
PR 14-MAY-1999; 99US-0134320.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.

```

PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142927.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 26-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.

```

```

PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157173.
PR 06-OCT-1999; 99US-0157753.
PR 07-OCT-1999; 99US-0157865.
PR 08-OCT-1999; 99US-0158029.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160815.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

Alignment Scores:

```

Pred. No.: 5.7e-46 Length: 561
Score: 410.00 Matches: 73
Percent Similarity: 85.32% Conservative: 20
Best Local Similarity: 66.97% Mismatches: 16
Query Match: 66.34% Indels: 0
DB: 21 Gaps: 0

```

US-09-786-715-8 (1-123) x AAC51522 (1-561)

```

QY 5 GIUGLUGLYGVALIIIEGLYVALIIISThrValAspGluTrpLysLeuGlnAsn 24
|||||
DB 103 GANAGAGACAGATGATCGCTGCCACCCGTTGACATGGAACGACGCTTCAAG 162
|||||
QY 25 ALALysAspSerLysLysLeuIIeValValAspPheThrAlaSerTrpCysGlyProCys 44
|||
DB 163 GCTATGATCAACAAACTCTGTGTGCTGATTCACGGCTCTTGTTGATGACCATGT 222
|||||
QY 45 ArgPheMetLarProValIIeAlaGluIIeAlaLysLysThrProGluLeuIIePheLeu 64
|||||
DB 223 CGTTTCATGCGTCCATCTTTCGTGATTTGGCTAAGAACTCTCAAGTGGCTTTTCCTC 282
|||||
QY 65 LysValAspValAspGluValArgProValAlaGluLutTrpSerIleGluAlaMetPro 84
|||||
DB 283 AAGTTTATACCTGATGATGATGAGTCGTCGCAAGTCATTTGGCGATACAGCGATGCCA 342
|||||
QY 85 ThrPheLeuPheLeuLysAspGlyGluIIeValAspLysValValGlyAlaSerLysAsp 104
|||||
DB 343 ACCTTCATGTTTGAAGGAAGGAGATTTTGACAAAGTGTGTGAGCCAGAAAGAT 402
|||||
QY 105 AspleuGlnAlaThrIleAlaLysHis 113
|||||
DB 403 GAGCTTCAGTCTACCATTTGCCAAACAC 429
|||||

```

RESULT 15
AAC34121
ID AAC34121 standard; DNA: 563 BP.
XX
AC AAC34121;
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 5524.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129645.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 28-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142380.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145293.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 17, 2003, 19:18:57 ; Search time 45.5839 Seconds
(without alignments)
1190.995 Million cell updates/sec

Title: US-09-786-715-8

Perfect score: 618

Sequence: 1 MAEVEGQYIGVHTDEWKL.....DDLQATIAKASVAAASS 123

Scoring table: BLOSUM62
Xgapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame.p2n.model -DEV=xlp
-O=/cgn2_1/uspt0.spool/US09786715/runat_11082003_150515_6083/app_query.fasta_1.1052
-DB=Issued_Patents_NA -QFMT=fastag -SUFFIX=ri -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=humana0.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09786715.eccn_1.175.4runat_11082003_150515_6083 -MCPu=6 -ICPU=3
-NO_MAMP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCOTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	392	63.4	393	4	US-09-540-014-5
2	392	63.4	653	1	US-08-181-271A-103
3	392	63.4	653	1	US-08-449-315-103
4	392	63.4	653	1	US-08-444-803-103
5	392	63.4	653	1	US-08-449-043-103
6	392	63.4	653	1	US-08-456-265A-103
7	392	63.4	653	1	US-08-455-416-103
8	392	63.4	653	1	US-08-455-244-103
9	392	63.4	653	1	US-08-454-876-103
10	392	63.4	653	2	US-08-457-364-103
11	392	63.4	653	2	US-08-456-262-103
12	392	63.4	653	2	US-08-456-240-103

13	392	63.4	653	2	US-08-455-736-103	Sequence 103, App
14	392	63.4	653	2	US-08-971-217-103	Sequence 103, App
15	392	63.4	653	3	US-09-350-600-103	Sequence 103, App
16	389	62.9	359	4	US-09-540-014-1	Sequence 1, Appl1
17	388	62.8	382	4	US-09-540-014-3	Sequence 3, Appl1
18	388	62.8	557	4	US-09-404-879A-88	Sequence 88, Appl1
19	388	62.8	557	4	US-09-338-933-88	Sequence 88, Appl1
20	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
21	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
22	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
23	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
24	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
25	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
26	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
27	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
28	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
29	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
30	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
31	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
32	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
33	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
34	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
35	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
36	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
37	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
38	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
39	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
40	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
41	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
42	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
43	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
44	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1
45	388	62.8	557	4	US-09-215-681-88	Sequence 88, Appl1

ALIGNMENTS

RESULT 1
US-09-540-014-5
; Sequence 5, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Calliau, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: wheat thioredoxin h cDNA
US-09-540-014-5

Alignment Scores:
Pred. No.: 6,18e-46
Score: 392.00
Length: 393
Matches: 65

Percent Similarity: 82.61% Conservative: 30
Best Local Similarity: 56.52% Mismatches: 20
Query Match: 63.43% Indels: 0
DB: 4 Gaps: 0

US-09-786-715-8 (1-123) x US-09-540-014-5 (1-393)

Oy 2 AlaGlValGluGluGluValIleGlyValHisThrValAspGluTrpLeuGln 21
Db 46 GCGGCGTGGGGGGGGGGAGGTGATCTCCGTCACAGCTGGAGCATGACATGCGAG 105
Oy 22 LeuGlnAsnAlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrpCys 41
Db 106 ATCAGAGGAGCCACGCGCCAGAGAGCTGGTGATGATGACTGATCATGATCATGATGATG 165
Oy 42 GlyProCysArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGluLeu 61
Db 166 GGACCATGCGCATTTATGCTGCTCCATTTTCTGCTGCGCAGAAAGTTCACAGCTGCT 225
Oy 62 IlePheLeuLysValAspValAspGluValArgProValAlaGluGluTrpSerIleGlu 81
Db 226 GTTTTCTCAAGGTCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 285
Oy 82 AlaMetProThrPheLeuPheLeuLysAspGluIleValAspLysValAlaGlyVal 101
Db 286 GCCATGCCACACCTTCCTGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 345
Oy 102 SerLysAspAspLeuGlnAlaThrIleAlaLysLysAlaSerAla 116
Db 346 ATCAAGGAGAGAGCTGACAGCAAGGTTGGCTCCACGCGCTGCC 390

RESULT 2
US-08-181-271A-103
Sequence 103, Application US/08181271A
Patent No. 5614395

GENERAL INFORMATION:

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Spertison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericka C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271A
FILING DATE: 13-JAN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-181-271A-103

Alignment Scores:

Pred. No.: 1,29e-45 Length: 653
Score: 392.00 Matches: 72
Percent Similarity: 83.04% Conservative: 21
Best Local Similarity: 64.29% Mismatches: 18
Query Match: 63.43% Indels: 1
DB: 1 Gaps: 0

US-09-786-715-8 (1-123) x US-08-181-271A-103 (1-653)

Oy 5 GluGluGluGlnValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsn 24
Db 75 GAGGAGGAGCAAGTTCGCTGCCACAGGTTGAGGATGAGAGTGAAGAGTACTTCAAGAA 134
Oy 25 AlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCys 44

Db 135 GGGCTTGAGACTAAGAAAGTGTGTGTGTCATTTTACTTCATGTCGCGSCCTTGC 194
QY 45 ArgPheMetaIaprovAlaIeuaIagIuIleAlaIySthrProgluIeuIlePheIeu 64
Db 195 CGTTTATTTGCCCAATTTCTTGTGACATTGCTAAGAAAGTGCATGTTATATTCCTC 254
QY 65 LysValAspValAspIuValArgProValAla-GluIuIyTserIleGluAlaMetPr 84
Db 255 AAGCTTGATGTTATGACTGAAGACTGTTTCAGCGGGAATGAGTGTGAGGCATGCC 314
QY 84 othrPheIeuPheIeuLysAspIyGluIleValAspLysValAlaIyAlaSerLysAs 104
Db 315 AACTTTGCTTCATTAAGATGAAGAAAGAGTGAAGAGTGTGTGTCACAAAGAAAGA 374
QY 104 pasPleuGluAlaThrIleAlaIySthrAlaSer 115
Db 375 GGAGTTGCAGACACCATAGTGAAGCATGCTGCT 408

RESULT 3
US-08-449-315-103
Sequence 103, Application US/08449315
Patent No. 5650305
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,315
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-449-315-103

Alignment Scores:
Pred. No.: 1,296-45 Length: 653
Score: 392.00 Matches: 72
Percent Similarity: 83.048 Conservative: 21
Best Local Similarity: 64.298 Mismatches: 18
Query Match: 63.436 Indels: 1
DB: 1 Gaps: 0

US-09-786-715-8 (1-123) x US-08-449-315-103 (1-653)

QY 5 GluIuGlyIeValIleGlyValAlaIySthrValAspIuIyLysLeuIleGluIleAsn 24
Db 75 GAGAGGAGCAAGTTCGCTGCCACAGGTTGAGAGCAAGTACTTACAGAA 134
QY 25 AlaIyAspSerLysIleuIleValAspPheThrAlaSerTrpGlyProGly 44
Db 135 GGGCTTGAGACTAAGAAAGTGTGTGTCATTTTACTTCATGTCGCGSCCTTGC 194
QY 45 ArgPheMetaIaprovAlaIeuaIagIuIleAlaIySthrProgluIeuIlePheIeu 64
Db 195 CGTTTATTTGCCCAATTTCTTGTGACATTGCTAAGAAAGTGCATGTTATATTCCTC 254
QY 65 LysValAspValAspIuValArgProValAla-GluIuIyTserIleGluAlaMetPr 84
Db 255 AAGCTTGATGTTATGACTGAAGACTGTTTCAGCGGGAATGAGTGTGAGGCATGCC 314
QY 84 othrPheIeuPheIeuLysAspIyGluIleValAspLysValAlaIyAlaSerLysAs 104

GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedlich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Sherilca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-449-043-103
Alignment Scores:
Pred. No.: 1.29e-45 Length: 653
Score: 392.00 Matches: 72
Percent Similarity: 83.04% Conservative: 21
Best Local Similarity: 64.29% Mismatches: 18
Query Match: 63.43% Indels: 1
DB: 1 Gaps: 0
US-09-786-715-8 (1-123) x US-08-449-043-103 (1-653)
QY 5 GUGUGUGYglnValIleGlyValIHisThrValAspGluTrpLysLeuGlnAsn 24
|||||
Db 75 GAGGAGGAGCAAGTGTTCGGCTGCCACAGCTTGAGGAATGAGCAACGACTCTCAAGAAA 134
QY 25 AlaLysAspSerLysLysLeuIleValAlaAspPheThrAlaSerTrpCysGlyProCys 44
|||||
Db 135 GCGCTGAGACTAAGAAAGCGTGGTGCATTTACGCTTCATGCTGCGGSCCTTGC 194
QY 45 ArgPheMetAlaProValLeuAlaGluIleAlaLysThrProGluLeuIlePheLeu 64
|||||
Db 195 CGTTTATTTGCCCAATTCCTTCTGCAATTCCTTAAGAAGATGCCCATGTTATATTCCTC 254
QY 65 LysValAspValAspGluValArgProValAla-gluGluTrpSerIleGluAlaMetPr 84
|||||
Db 255 AAGGTTGATGTTGATGACGAGAGCTGTTTCAGCGGAATGAGTGTGAGGCAATGCGC 314
QY 84 oThrPheLeuPheLeuLysAspGlyGluIleValAspLysValAlaGlyAlaSerLysAs 104
|||||
Db 315 AACCTTTGCTTCATTAAAGATGAAAGAAAGGACAGAGTGTGTGCGCAAGAAAGA 374
QY 104 pasPleuGlnAlaThrIleAlaLysHisAlaSer 115
|||||
Db 375 GGAAGTTCACACAGACCATGATGACATGCTGCT 408
RESULT 6
US-08-456-265A-103
Sequence 103, Application US/08456265A
Patent No. 5767369
GENERAL INFORMATION:
APPLICANT: Alexander, Danny C.
APPLICANT: Ryals, John A.
APPLICANT: Goodman, Robert M.
APPLICANT: Stinson, Jeffrey R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005

CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,265A
FILING DATE: 31-MAY-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-456-265A-103

Alignment Scores:
Pred. No.: 1,296-45 Length: 653
Score: 392.00 Matches: 72
Percent Similarity: 83.04% Conservative: 21
Best Local Similarity: 64.29% Mismatches: 18
Query Match: 63.43% Indels: 1
DB: 1 Gaps: 0
US-09-786-715-8 (1-123) x US-08-456-265A-103 (1-653)
QY 5 GluGluGlyGlnValIleGlyValHisThrValAspGluTrpLysLeuGlnAsn 24
|||||
DB 75 GAGGAGGACCAAGTGGCTGCCCAAGTTGAGATGCAAGACTACTTCAAGAA 134
GAGGAGGACCAAGTGGCTGCCCAAGTTGAGATGCAAGACTACTTCAAGAA 134
QY 25 AlalysAspSerLysLeuIleValValAspPheTrpAlaSerTrpCysGlyProCys 44
|||||
DB 135 GCGCTTGAGACTAGAAACTGGTGGTCTGCTTACTGCTTCTGCTGCGGSCCTTGC 194
GCGCTTGAGACTAGAAACTGGTGGTCTGCTTACTGCTTCTGCTGCGGSCCTTGC 194
QY 45 ArgPheMetAlaProValLeuAlaGluIleAlaLysLysTrpProGluLeuIlePheLeu 64
|||||
DB 195 GCTTTATTGCCCAATCTGCTGACATGCTAGAGAGATGCCCATGTTATTCTCTC 254
GCTTTATTGCCCAATCTGCTGACATGCTAGAGAGATGCCCATGTTATTCTCTC 254
QY 65 LysValAspValAspGluValArgProValAla-GluGluTrpSerIleGluAlaMetCpr 84
|||||
DB 255 AAGGTTGATGTTGATGAGACTGAGACGCTTTCAGCGGGAATGAGACTGGAGCGCATGCC 314
AAGGTTGATGTTGATGAGACTGAGACGCTTTCAGCGGGAATGAGACTGGAGCGCATGCC 314
QY 84 CThrPheLeuPheLeuLysAspGlyGluIleValAspLysValGlyAlaSerLysAs 104
|||||
DB 315 AACCTTTGCTTCTCATTAAGATGGAAGAAAGATGGACAGACTTGTGTGTCAGAAAGAA 374
AACCTTTGCTTCTCATTAAGATGGAAGAAAGATGGACAGACTTGTGTGTCAGAAAGAA 374
QY 104 PAspLeuGlnAlaThrIleAlaLysHisAlaSer 115
|||||
DB 375 GGAGTTGCAGCAGACCAATAGTGAAGCAGTCGTCT 408
GGAGTTGCAGCAGACCAATAGTGAAGCAGTCGTCT 408
RESULT 7
US-08-455-416-103
; Sequence 103, Application US/08455416
; Patent No. 5777200
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Spertson, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Sherilca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-455-416-103

Alignment Scores:
Pred. No.: 1.29e-45 Length: 653
Score: 392.00 Matches: 72
Percent Similarity: 83.04% Conservative: 21
Best Local Similarity: 64.29% Mismatches: 18
Query Match: 63.43% Indels: 1
DB: 1 Gaps: 0

US-09-786-715-8 (1-123) x US-08-455-416-103 (1-653)

QY 5 GluGluGlyGlnValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsn 24
|||||
DB 75 GAGGAGGAGCAAGTTCGGCTCCACCAAGCTTGAGAGAAAGACAGTACTTCAAGAAA 134
QY 25 AlAlAspSerLysLysLeuIleValAspPheThrAlaSerTrpCysGlyProCys 44
|||||
DB 135 GCGGTGAGACTAGAAACACTGGTGGTGGTCACTTTACCTTCATCGTCCGSSCCTTGC 194
QY 45 ArgPheMetAlaProValLeuAlaGluIleAlaLysThrProGluLeuIlePheLeu 64
|||||
DB 195 CGTTTATTGCCCATTCCTGCACTTGAAGATGCTAAAGATGCCCATGTATATTCCTC 254
QY 65 LysValAspValAspGluValArgProValAla-GluGluTrpSerIleGluAlaMetPr 84
|||||
DB 255 AAGCTTGATGTTGATGACGAGACTGTTTCACCGGAAAGGAGTGAGGAGCAATGCC 314
QY 84 oThrPheLeuPheLeuLysAspLysLysLysLysLysLysLysLysLysLysLys 104
|||||
DB 315 AACCTTTGCTTCATTAAAGATGAAAGAAAGAGGACAGAGTGTGTCCTCAAGAAA 374
QY 104 pasPleuGlnAlaThrIleAlaLysHisAlaSer 115
|||||
DB 375 GGAGTTGCAGACAGCACCATAGTGAACATGCTGCT 408

RESULT 8
US-08-455-244-103
Sequence 103, Application US/08455244
Patent No. 5789214
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesling, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-455-244-103

Alignment Scores:
Pred. No.: 1 296-45 Length: 653
Score: 392.00 Matches: 72
Percent Similarity: 83.04% Conservative: 21
Best Local Similarity: 64.29% Mismatches: 18
Query Match: 63.43% Indels: 1
DB: 1 Gaps: 0

US-09-786-715-8 (1-123) x US-08-455-244-103 (1-653)

QY 5 GlnGlnGlnGlnValIleGlnValHisThrValAspGluTrpLysLeuGlnLeuGlnAsn 24
Db 75 GAGAGGAGACAAAGTTCGGGTGCACAGAGTTGAGGATGAGACGAGTACTCAAGAA 134
QY 25 AlAlAspSerLysLysLeuIleValAlaAspPheThrAlaSerTTPCysGlyProCys 44
Db 135 GGCCTTAGACTAGAAACGTGGTGTGCTGATTTTACTGCTTCATGGTGGGSCCTTGC 194
QY 45 ArpPheMetIaIaProValLeuAlaGlnIleAlaLysLysThrProGlnLeuIlePheLeu 64
Db 195 CGTTTATGGCCCAATTCTTGCTGACATTCGTAAAGAGATGCCCATGTTATATCTCTC 254

QY 65 LysValAspValAspGluValArpProValAla-GlnGlnTrpSerIleGlnAlaMetPr 84
Db 255 AAGGTTGATGTGGATGAACCTGAGACTGTTTCAGCGGGAATGAGATGTGAGCGCATGCC 314
QY 84 OthPheLeuPheLeuLysAspGlyGlnIleValAlaAspLysValAlaGlyAlaSerLysAs 104
Db 315 AACTTTCCTTCATTAAAGATGGAAGAAGATGGACAGAGTTGTTGGTCCCAAGAAAGA 374
QY 104 PAspLeuGlnAlaThrIleAlaLysHisAlaSer 115
Db 375 GGAGTTGACGACGACCATAGTGAAGCATGCTGCT 408

RESULT 9
US-08-454-876-103
Sequence 103 Application US/08454876
Patent No. 3804693
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847

SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-456-240-103

Alignment Scores:
Pred. No.: 1,29e-45 Length: 653
Score: 392.00 Matches: 72
Percent Similarity: 83.04% Conservative: 21
Best Local Similarity: 64.29% Mismatches: 18
Query Match: 63.43% Indels: 1
Gaps: 0

US-09-786-715-8 (1-123) x US-08-456-240-103 (1-653)

QY 5 GluGluGlyGlnValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsn 24
|||||
Db 75 GAGGAGGAGCAAGAGTTCGGCTGCCACAGAGTTGAGAGATGCAAGAGTACTTCAAGAAA 134
|||||

QY 25 AlAlAspSerLysLysLeuIleValValAspPheThrAlaSerTPCysGlyProCys 44
.....
Db 135 GGCCTTACAGCTAAGAACTGGTGGTGCATTTTCTGCTGATGCTGGGSCCTTGC 194
|||||

QY 45 ArpPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGluLeuIlePheLeu 64
|||||
Db 195 CGTTTATTCGCCCAATCTCTGTCGACATTCCTAAGAAAGATGCCCATGTTATTTCTC 254
|||||

QY 65 LysValAspValAspGluValArgProValAla-GluGluTrpSerIleGluAlaMetPr 84
|||||
Db 255 AAGGTGATGTGATGATGAAGAGTGTTCACGGGAAATGAGGTGGAGCAATGCC 314
|||||

QY 84 othrPheLeuPheLeuLysAspGlyGluIleValAspLysValValGlyAlaSerLysAs 104
|||||
Db 315 AACTTTGCTCTCTTAAGATGGAAGAAGTGAAGAGTGTGTGCTGCCAAGAAA 374
|||||

QY 104 PAspLeuGlnAlaThrIleAlaLysHisAlaSer 115
|||||
Db 375 GGAAGTTCACAGACCATAGTGAAGATGCTGCT 408
|||||

RESULT 13
US-08-455-736-103
Sequence 103, Application US/08455736
Patent No. 5880328

GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Melns, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA

ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,736
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-1994
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-455-736-103

Alignment Scores:
Pred. No.: 1,29e-45 Length: 653
Score: 392.00 Matches: 72

Percent Similarity: 83.04% Conservative: 21
 Best Local Similarity: 64.29% Mismatches: 18
 Query Match: 63.43% Indels: 1
 DB: 2 Gaps: 0

US-09-786-715-8 (1-123) x US-08-455-736-103 (1-653)

OY 5 GUGUGUGLGNValIIleGlyValHsthrValAspGluTrpLysLeuGlnLeuGlnasn 24
 |||||
 DB 75 GAGGAGGACACAGTGTTCGCTGCCACAAAGTTGGAGAAAGAGAGAGTACTTCAAGAAA 134
 OY 25 AlalysasSerLysLeuIleValAlaspheThralaSerTrpCysGlyProCys 44
 :
 DB 135 GCCGTTGAGACTAAAGAACTGGTGGTGCATTTTACTGCTCATGTGCGGSGCTTGC 194
 OY 45 ArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGluLeuIlePheLeu 64
 |||||
 DB 195 CGTTTATTTGCCCAATTCCTGTCATTCCTAAGAGATGCCCATGTATATTTCTC 254
 OY 65 LysValaspValaspGluValArgProValAla-GluGluTrpSerIleGluAlaMetPr 84
 |||||
 DB 255 AAGTTGATGTTGATGAACAGTGTTCACGGCGGATGAGTGTGGAGGCAATGCC 314
 OY 84 OthPheLeuPheLeuLysaspGlyGluIleValaspLysValAlaGlyAlaSerLysAs 104
 |||||
 DB 315 AACTTTGTCTTCATTAAAGATGAAAGAAAGTGCACAGAGTTGTTGGTCCAAAGAAA 374
 OY 104 pasPheGlnAlaThrIleAlaLysHisAlaSer 115
 :
 DB 375 GGAGTTGCAGCAGACCATAGTGAACATGCTGCT 408

RESULT 14

US-08-971-217-103
 Sequence 103 Application US/08971217
 Patent No. 5942662

GENERAL INFORMATION:
 APPLICANT: Ryals, John A.
 APPLICANT: Harms, Christian
 APPLICANT: Friedrich, Leslie
 APPLICANT: Beck, James
 APPLICANT: Uknes, Scott
 TITLE OF INVENTION: INDUCIBLE HERBICIDE RESISTANCE
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5942662artis Corporation
 STREET: 3054 Cornwalls Road, P.O. Box 12257
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/971,217
 FILING DATE:

CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/457,364
 FILING DATE: 31-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/181,271
 FILING DATE: 13-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,847
 FILING DATE: 6-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/632,441
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8587
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 653 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-971-217-103

Alignment Scores:
 Pred. No.: 1.29e-45 Length: 653
 Score: 392.00 Matches: 72
 Percent Similarity: 83.04% Conservative: 21
 Best Local Similarity: 64.29% Mismatches: 18
 Query Match: 63.43% Indels: 1
 DB: 2 Gaps: 0

US-09-786-715-8 (1-123) x US-08-971-217-103 (1-653)

OY 5 GUGUGUGLGNValIIleGlyValHsthrValAspGluTrpLysLeuGlnLeuGlnasn 24
 |||||
 DB 75 GAGGAGGACACAGTGTTCGCTGCCACAAAGTTGGAGAAAGAGAGAGTACTTCAAGAAA 134
 OY 25 AlalysasSerLysLeuIleValAlaspheThralaSerTrpCysGlyProCys 44
 :
 DB 135 GCCGTTGAGACTAAAGAACTGGTGGTGCATTTTACTGCTCATGTGCGGSGCTTGC 194
 OY 45 ArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGluLeuIlePheLeu 64
 |||||
 DB 195 CGTTTATTTGCCCAATTCCTGTCATTCCTAAGAGATGCCCATGTATATTTCTC 254

QY 65 LysValAspValAspGluValArgProValAla-GluGluTyrSerIleGluAlaMetPr 84
Db 255 AAGGTGATGTTGATGAAAGACATGTTTACGCGGAAATGAGTGTGAGGCAATGCC 314
QY 84 othrPheLeuPheLeuLysAspGlyGluIleValAspLysValAlaGlyLysSerLysAs 104
Db 315 AACCTTTGCTTCATTAAAGATGGAAGAAAGAGTGCAGACAGATTGTTGCCAAGAAAGA 374
QY 104 PASPLEUGLNALETALALALYSHISLASER 115
Db 375 GGAAGTTCACACACACATAGTGAAGCATGCTGCT 408
RESULT 15
US-09-350-600-103
Sequence 103, Application US/09350600
Patent No. 6262342
GENERAL INFORMATION:
APPLICANT: Meins, Frederick
APPLICANT: Shinshi, Hideaki
APPLICANT: Menzler, Herman
APPLICANT: Hofsteenge, Jan
APPLICANT: Ryals, John
APPLICANT: Sperisen, Christoph
TITLE OF INVENTION: DNA SEQUENCES ENCODING POLYPEPTIDES
TITLE OF INVENTION: HAVING BETA-1,3-GLUCANASE ACTIVITY
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6262342artis Corporation
STREET: 3054 Cornwallis Road, P.O. Box 12257
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,600
FILING DATE: US/09/350,600
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/971,217
FILING DATE: 14-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,364
FILING DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504

FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/381,443
FILING DATE: 18-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/353,312
FILING DATE: 17-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/226,303
FILING DATE: 29-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-198250
TELEPHONE: (919)541-8587
TELEFAX: (919)341-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-350-600-103
Alignment Scores:
Pred. No.: 1 29e-45 length: 653
Score: 392.00 Matches: 72
Percent Similarity: 83.04% Conservative: 21
Best Local Similarity: 64.29% Mismatches: 18
Query Match: 63.43% Indels: 1
Gaps: 0
US-09-786-715-8 (1-123) x US-09-350-600-103 (1-653)
QY 5 GluGluGlyGlnValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsn 24
Db 75 GAGGAGGACAAAGTGTGCGCTCCACAAAGTTGAGGAAGAAAGCAAGTACTTCAAGAAA 124
QY 25 AlAlAspSerLysLysLeuIleValAlaAspPheThrLysSerTrpGlyProGly 44
Db 135 GCGGTGAGACTAGAAAGTGTGGTGGTGGATTACTGCTTCACTGCTTCAAGGSCCTTGC 194
QY 45 ArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGluLeuIlePheLeu 64
Db 195 CGTTTATTCGCCCAATTCCTTCTGCTGACATTCCTAAGAAAGTCCCATGTTATATTCCTC 254
QY 65 LysValAspValAspGluValArgProValAla-GluGluTyrSerIleGluAlaMetPr 84
Db 255 AAGGTGATGTTGATGAAAGACATGTTTACGCGGAAATGAGTGTGAGGCAATGCC 314
QY 84 othrPheLeuPheLeuLysAspGlyGluIleValAspLysValAlaGlyLysSerLysAs 104
Db 315 AACCTTTGCTTCATTAAAGATGGAAGAAAGAGTGCAGACAGATTGTTGCCAAGAAAGA 374

QY 104 paspleuglnAlaThrIleAlaIysHisAlaSer 115
:::||||| | ||| | |||||:::
Db 375 GGAGTTCACACACCATAGTGAAGCATGCTGCT 408

Search completed: August 17, 2003, 21:45:28
Job time : 51.5839 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 19:25:47 ; Search time 143.373 Seconds
(without alignments)
1919.938 Million cell updates/sec

Title: US-09-786-715-8

Perfect score: 618
Sequence: 1 MAEEVEGCVIGVHTDEWKL.....DLQATIAKHAASVAASSS 123

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1504479 seqs, 1118970152 residues

Total number of hits satisfying chosen parameters: 3008958

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DEV=xlp
-Q=/cgn2_1/USPTO/US09786715/runat_11082003_150515_6129/app_query.fasta_1.1052
-DB=Published_Applications_NA -QMT=fastap -SUFFIX=rmpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blsum62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USRR=US09786715 @cgn_1.1.560 @runat_11082003_150515_6129
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEIOBERT -NEG_SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FCAPOP=6 -FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PTI_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCRTS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	565	91.4	390	US-09-878-574-1462	Sequence 1462, Ap

2	515	83.3	392	10	US-09-878-574-104	Sequence 104, App
3	425	68.8	402	10	US-09-878-574-3723	Sequence 3723, Ap
4	413	66.8	270	10	US-09-878-574-13445	Sequence 13445, A
5	411	66.5	3888	9	US-09-897-898-10	Sequence 10, Appl
6	410	66.3	345	10	US-09-938-842A-163	Sequence 163, App
7	410	66.3	3129	9	US-09-897-898-7	Sequence 5, Appl1
8	406	65.7	3888	9	US-09-897-898-7	Sequence 7, Appl1
9	406	65.7	540	12	US-10-349-782-12	Sequence 5, Appl1
10	392	63.4	393	12	US-10-091-841-5	Sequence 12, Appl
11	389	62.9	369	12	US-10-194-865-8	Sequence 5, Appl1
12	389	62.9	369	12	US-10-091-841-1	Sequence 8, Appl1
13	388	62.8	382	12	US-10-091-841-3	Sequence 1, Appl1
14	380.5	61.6	360	10	US-09-938-842A-164	Sequence 164, Appl
15	377	61.0	659	12	US-10-349-782-9	Sequence 9, Appl1
16	374	60.5	357	10	US-09-938-842A-1736	Sequence 1736, Ap
17	374	60.5	357	14	US-10-323-362-1	Sequence 1, Appl1
18	364	58.9	260	10	US-09-878-574-12941	Sequence 12941, A
19	361	58.4	267	10	US-09-878-574-13137	Sequence 13137, A
20	340	55.0	272	10	US-09-878-574-12181	Sequence 12181, A
21	302	48.9	297	12	US-10-349-782-11	Sequence 11, Appl
22	298	48.2	277	10	US-09-878-574-8135	Sequence 8135, Ap
23	286	46.3	370	10	US-09-878-574-3169	Sequence 3169, Ap
24	279	45.1	250	9	US-09-923-876-1288	Sequence 1288, Ap
25	275	44.5	268	10	US-09-938-842A-225	Sequence 225, Ap
26	268	43.4	402	10	US-09-938-842A-795	Sequence 795, App
27	268	43.4	613	9	US-09-770-149-855	Sequence 855, App
28	255	41.3	456	10	US-09-924-035A-677	Sequence 677, App
29	254	41.1	390	10	US-09-938-842A-2688	Sequence 2688, Ap
30	228	36.9	440	9	US-09-770-444-914	Sequence 914, App
31	225	36.4	357	10	US-09-938-842A-147	Sequence 147, App
32	224	36.2	413	14	US-10-102-524-1396	Sequence 1396, Ap
33	224	36.2	418	10	US-09-796-692-3641	Sequence 3641, Ap
34	224	36.2	418	14	US-10-040-862-3641	Sequence 3641, Ap
35	224	36.2	464	10	US-09-998-558-1059	Sequence 1059, Ap
36	224	36.2	479	11	US-09-535-459-1145	Sequence 1145, Ap
37	224	36.2	536	14	US-10-066-543-65	Sequence 65, Appl
38	224	36.2	540	10	US-09-920-300A-1247	Sequence 1247, Appl
39	224	36.2	540	13	US-10-083-548-1247	Sequence 1247, Ap
40	224	36.2	557	10	US-09-884-441-88	Sequence 88, Appl
41	224	36.2	557	11	US-09-907-969-88	Sequence 88, Appl
42	224	36.2	557	14	US-10-198-053-88	Sequence 88, Appl
43	224	36.2	568	11	US-09-535-459-1139	Sequence 1139, Ap
44	224	36.2	570	11	US-09-535-459-1149	Sequence 1149, Ap
45	224	36.2	594	10	US-09-884-441-87	Sequence 87, Appl

ALIGNMENTS

RESULT 1

US-09-878-574-1462
Sequence 1462, Application US/09878574

Patent No. US2002010548A1
GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

PRIOR FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 1462

LENGTH: 390

TYPE: DNA

ORGANISM: Glycine max

OTHER INFORMATION: Clone ID: LIB3028-037-Q1-B1-F11

US-09-878-574-1462

Alignment Scores:

Pred. No.:

1.51e-74

Length:

390

Score: 565.00 Matches: 111
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 91.42% Indels: 0
DB: 10 Gaps: 0

US-09-786-715-8 (1-123) x US-09-878-574-1462 (1-390)

QY 1 MetalagluValagluValIleGlyValHisThrValAspGluTrpLysLeu 20
DB 57 ATGGCTGAAGTGAAGGACAGGTGATGCGCTCCACACCGTTGATGAGTGAAGCTG 116
QY 21 GluLeuGlnAsnAlaLysAspSerLysLeuIleValValAspPheThrAlaSerTrp 40
DB 117 CAATCCAGATGGAAGAAAGACTCCAAAAGTGTGTTGGTGGATTTACTGCTCTCGG 176
QY 41 CysGlyProCysArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGlu 60
DB 177 TGTGCTCCAGCCGTTTATGCCCCAGTTCTTCACAGATTGCCAAAAGAAACTCCTGAA 236
QY 61 LeuIlePheLeuLysValAspLysValAspGluValArgProValAlaGluGluTrpSerIle 80
DB 237 TTGATCTTCTCAAGTGAATGATGATGAGTGAAGGCTGTGCTGAGAAATATTCATT 296
QY 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyLysLeuIleValAspLysValGly 100
DB 297 GAGGCCATGCCAACCTTCTCTCTTGTGAAGATGCGAGATCGGACAAAGTGTGTGT 356
QY 101 AlaSerLysAspAspLeuGlnAlaThrIleAla 111
DB 357 GCTAGTAAGATGACCTTCAAGCCACCATGACC 389

RESULT 2

US-09-878-574-104
Sequence 104, Application US/09878574
Patent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878, 574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333, 535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 104
LENGTH: 392
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-056-Q1-B1-B3
US-09-878-574-104

Alignment Scores:

Pred. No.: 4,1e-67
Score: 515.00
Percent Similarity: 92.31%
Best Local Similarity: 83.76%
Query Match: 83.33%

DB: 10

US-09-786-715-8 (1-123) x US-09-878-574-104 (1-392)

QY 5 GluGluGlnValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsn 24
DB 12 GAAGAGGAGTGAAGTGTGCGCGTCCACACCGTTGATCGGAAACCACTGCAGAAAT 71
QY 25 AlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCys 44
DB 72 GGAAGAAGACTCCAAAAGATGATGTTGATTTTACTGCTTCCTGCTGTGCTCATGC 131

QY 45 ArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGluLeuIlePheLeu 64
DB 132 CGTTTATTTGCCCCAGTTCTTGCGCAGATGCTAGCATCTCTCTCAAGATCTTCTC 191
QY 65 LysValAspValAspGluValArgProValAlaGluGluTrpSerIleGluAlaMetPro 84
DB 192 AAGGTGATGTGATGATGAGTGAAGGCGCTGTGCTGAGAAATTCATTTAGGCGCATGCCA 251

QY 85 ThrPheLeuPheLeuLysAspGlyLysLeuIleValValAspLysValGlyAlaSerLysAsp 104
DB 252 ACCTTCTCTTCTTGAAGATGCGAAGATGCTGATGATGATGATGATGATGATGATGATG 311

QY 105 AspLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAlaLaser 121
DB 312 GAGCTGCACTCAACCATGACCAAGCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 362

RESULT 3

US-09-878-574-3723
Sequence 3723, Application US/09878574
Patent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878, 574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333, 535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 3723
LENGTH: 402
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-006-Q1-B1-F8
US-09-878-574-3723

Alignment Scores:

Pred. No.: 1,01e-53
Score: 425.00
Percent Similarity: 86.49%
Best Local Similarity: 69.37%
Query Match: 68.77%

DB: 10

US-09-786-715-8 (1-123) x US-09-878-574-3723 (1-402)

QY 5 GluGluGlnValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsn 24
DB 49 GAAGAGGAGACAGATGCGTGTCCACACCGTGAAGAGTGAAGAAATCTCAAGAAAG 108
QY 25 AlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCys 44
DB 109 GGAAGAAGACTCCAAAAGATGATGTTGATTTTACTGCTTCCTGCTGTGCTCATGC 168
QY 45 ArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGluLeuIlePheLeu 64
DB 169 CGTTTCTTCCCAATTTCTTGCAAGATGCTTAAGAAGTTGCCGAATGACCTTCTC 228
QY 65 LysValAspValAspGluValArgProValAlaGluGluTrpSerIleGluAlaMetPro 84
DB 229 AAGGTGATGTGATGATGATGAGACGTTTCCACACAGTGGGAATGTAGGCTATGCCA 288
QY 85 ThrPheLeuPheLeuLysAspGlyLysLeuIleValValAspLysValGlyAlaSerLysAsp 104
DB 289 ACCTTCTCTTCTTGAAGATGCGAAGATGCTGATGATGATGATGATGATGATGATGATG 348
QY 105 AspLeuGlnAlaThrIleAlaLysHisAlaSer 115
DB 349 GAGCTGCAATTTGACCTTACGACGACGATGCGCA 381

PRIOR FILING DATE: 1997-05-27

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

NUMBER OF SEQ. ID NOS: 24			
SOFTWARE: patentin Ver. 2.1			
SEQ ID NO 5			
LENGTH: 3129			
TYPE: DNA			
ORGANISM: Arabidopsis thaliana			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (1555)..(1896)			
US-09-897-898-5			
Alignment Scores:			
Pred. No.:	3.44e-50		
Score:	410.00		
Percent Similarity:	85.32%		
Best local Similarity:	66.97%		
Query Match:	66.34%		
DB:	9		
	Gaps:		
US-09-786-715-8 (1-123) x US-09-897-898-5 (1-3129)			
QY	5	GlutluGlglglnValIleGlyValHisThrValaspGluTrpLysleuGlnIleuAsn	24
DB	1564	GAGACAGACACAGATGATCGCTGCCACACCTTGACAGATGAGACAGACACTTCAGAG	1623
QY	25	AlalysaspSerLysLysLeuIleValValaspPheThrAlaSerTPCyGlyProCys	44
DB	1624	GCTPMTAAMTCCAAACACTCTGTGTGTGTTATTTCACGGCTTCTGTGTGACCATGT	1683
QY	45	ArgPheMetIaPProValIleuAlaGluIleAlaLysIsthrProGluIleuIlePheLeu	64
DB	1684	CGTTTCATCGCTCCATTCCTTGTGATTTGGCTAAGAACTTCTTAACGTCCTTTCTC	1743
QY	65	LysValaspValaspGluValArgProValAlaGluGluTrpSerIleGluAlaMetPro	84
DB	1744	AAGGTGATTAAGTGAATGAAGTCGTCGCAAGTGAATGGCGATACAGCGATGCCA	1803
QY	85	ThrpheLeuPheLeuLysaspGlyGluIleValaspLysValAlaGlyAlaSerLysasp	104
DB	1804	ACCTTCATGTTTTTGAAGGAGGAGATTTTGGACAAAGTTGTTGGAGCCAGAAAGAT	1863
QY	105	AspLeuGlnAlaThrIleAlaLysHis	113
DB	1864	GAGCTTCAGTCTACCATTTGCCAAACAC	1890
RESULT 8			
US-09-897-898-7			
Sequence 7, Application US/09897898			
Patent No. US20020037303A1			
GENERAL INFORMATION:			
APPLICANT: DECKERS, HARM M.			
APPLICANT: VAN ROOIJEN, GIJS			
APPLICANT: BOOTHE, JOSEPH			
APPLICANT: GOLD, JANIS			
APPLICANT: MOLONEY, MAURICE M.			
APPLICANT: DALMIA, BIPIN K.			
TITLE OF INVENTION: THIODEDOLIN AND THIODEDOLIN REDUCTASE CONTAINING OIL			
TITLE OF INVENTION: BODY BASED PRODUCTS			
FILE REFERENCE: 034547/0104			
CURRENT APPLICATION NUMBER: US/09/897,898			
CURRENT FILING DATE: 2001-09-21			
PRIOR APPLICATION NUMBER: 09/577,147			
PRIOR FILING DATE: 2000-05-24			
PRIOR APPLICATION NUMBER: 09/448,600			
PRIOR FILING DATE: 1999-11-24			
PRIOR APPLICATION NUMBER: 09/084,777			
PRIOR FILING DATE: 1998-05-27			
PRIOR APPLICATION NUMBER: 60/047,753			
PRIOR FILING DATE: 1997-05-27			
PRIOR APPLICATION NUMBER: 60/047,779			
PRIOR FILING DATE: 1997-05-28			
PRIOR APPLICATION NUMBER: 60/075,863			
PRIOR FILING DATE: 1998-02-25			

Score: 392.00 Matches: 65
 Percent Similarity: 82.61% Conservative: 20
 Best Local Similarity: 56.52% Mismatches: 30
 Query Match: 63.43% Indels: 0
 DB: 12 Gaps: 0

US-09-786-715-8 (1-123) x US-10-091-841-5 (1-393)

QY 2 AlaGluValIGluGluGlnValIleGluValHisThrValAspGluTrpLysLeuGln 21
 DB 46 GCGGGGCGGGGGGGGGAGGTGATCTCCGTCACACCGCTGGACAGTCAGTCAG 105
 QY 22 LeuGlnAsnAlaLysAspSerLysLeuIleValAlaAspPheThrAlaSerTrpCys 41
 DB 106 ATCGAGGAGCCCAACGCCCAAGAGCTGGTGATGACTTCATCAGCATCATGCTGC 165
 QY 42 GLYPGCGATGPhMetAlaProValLeuAlaGluIleAlaLysLysThrProLysLeu 61
 DB 166 GGACCATCCCGCATTTATGCTCCATTTTGTGCTGCTGCCAAGAGTTCCACCTGCT 225
 QY 62 IlePheLysValAspValAspLysValArgProValAlaGluGluTrpSerIleGlu 81
 DB 226 GTTTTCCCAAGTCGAGCTGATGACTGAAGCCCATTCGTCAGCATTCAGCTCGAG 285
 QY 82 AlaMetProThrPheLeuPheLysAspGluIleValAlaAspLysValAlaGlyAla 101
 DB 286 GCCATGCCCAACCTTCCTGTCATGAGAGAGACGTCAGACAGGAGGTTGTCGAGCT 345
 QY 102 SerLysAspAspLysLeuGlnAlaThrIleAlaLysHisAlaSerAla 116
 DB 346 ATCAAGGAGAGCTGACGACCAAGGTTGGCTCCACGGGGCTGCC 390

RESULT 11

US-10-194-885-8
 ; Sequence 8, Application US/10194885
 ; Publication No. US20030135678A1

GENERAL INFORMATION:

APPLICANT: Wong, J. H.

APPLICANT: Cho, Myeong-Je

APPLICANT: Lemaux, Peggy G.

APPLICANT: Buchanan, Bob

TITLE OF INVENTION: TRANSGENIC PLANTS WITH ELEVATED

FILE REFERENCE: 41627200800

CURRENT APPLICATION NUMBER: US/10/194,885

PRIOR FILING DATE: 2002-07-12

PRIOR APPLICATION NUMBER: 60/307,006

PRIOR FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: 09/538,864

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/126,736

PRIOR FILING DATE: 1999-03-29

NUMBER OF SEQ ID NOS: 55

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 369

TYPE: DNA

ORGANISM: Barley

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(369)

US-10-194-885-8

Alignment Scores:

Pred. No.: 1,99e-48 Length: 369
 Score: 389.00 Matches: 64
 Percent Similarity: 85.32% Conservative: 29
 Best Local Similarity: 58.72% Mismatches: 16
 Query Match: 62.94% Indels: 0
 DB: 12 Gaps: 0

US-09-786-715-8 (1-123) x US-10-194-885-8 (1-369)

QY 8 GlnValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsnAlaLysasp 27
 DB 37 GAGGTGATCTCGCTCCAGAGCTCGAGAGAGTGGACCATGACATGAGAGGCCCAACCC 96
 QY 28 SerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCysArgPheMet 47
 DB 97 GCCAAGAGCTGGTGGTGTGACTTCACTGCATCATGTGTGCGGACCATGCCGCTCATG 156
 QY 48 AlaProValLeuAlaGluIleAlaLysLysThrProGluLeuIlePheLysValAsp 67
 DB 157 GCTCCAGTTTCGCGATGATCTGCCAAGAGTTCCCAAAATGCTGTTTCTCCTCAAGCTCGAC 216
 QY 68 ValAspGluValArgProValAlaGluGluTrpSerIleGluAlaMetProThrPheLeu 87
 DB 217 GTGATGAGAGTGAAGAGAGCTGATGCTGAGCAATTCATGCTGAGGCCATGCCATGCTCCTG 276
 QY 88 PheLeuLysAspGluIleValAlaLysLysValAlaGlyAlaSerLysAspAspLeuGln 107
 DB 277 TTCATGAAGAGAGAGAGAGCTCAAGAGAGGTTGTGCGAGCTATATCAAGAGAGACTGACC 336
 QY 108 AlaThrIleAlaLysHisAlaSerAla 116
 DB 337 GCCAAGGTTGGGCTTCACGGCGGGGCC 363

RESULT 12

US-10-091-841-1

; Sequence 1, Application US/10091841

; Publication No. US20030150010A1

GENERAL INFORMATION:

APPLICANT: Cho, Myeong-Je

APPLICANT: Del Val, Greg

APPLICANT: Calliau, Maxime

APPLICANT: Lemaux, Peggy G.

APPLICANT: Buchanan, Bob B.

TITLE OF INVENTION: NADP-Thioredoxin and

FILE REFERENCE: 2001-0701.30

CURRENT APPLICATION NUMBER: US/10/091,841

PRIOR FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: 09/540,014

PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: US 60/127,198

PRIOR FILING DATE: 1999-03-31

PRIOR APPLICATION NUMBER: US 60/169,162

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: US 60/177,740

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US 60/177,739

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 369

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: barley thioredoxin h cDNA

US-10-091-841-1

Alignment Scores:

Pred. No.: 1,99e-48 Length: 369
 Score: 389.00 Matches: 64
 Percent Similarity: 85.32% Conservative: 29
 Best Local Similarity: 58.72% Mismatches: 16
 Query Match: 62.94% Indels: 0
 DB: 12 Gaps: 0

US-09-786-715-8 (1-123) x US-10-091-841-1 (1-369)

QY 8 GlnValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsnAlaLysasp 27
 DB 37 GAGGTGATCTCGCTCCAGAGCTCGAGAGAGTGGACCATGACATGAGAGGCCCAACCC 96

[illegible]

RESULT 13
US-10-091-841-3

```

Sequence, Application US/10091841
Publication No. US20030150010A1
GENERAL INFORMATION:
APPLICANT: Cho, Myeong-Je
APPLICANT: Del Val, Greg
APPLICANT: Calliau, Maxime
APPLICANT: Lemaux, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: Batley Gene for Thioredoxin and
TITLE OF INVENTION: NADP-Thioredoxin Reductase
FILE REFERENCE: 2001-0701, 30
CURRENT APPLICATION NUMBER: US/10/091,841
CURRENT FILING DATE: 2002-03-05
PRIORITY APPLICATION NUMBER: 09/340,014
PRIORITY FILING DATE: 2000-03-31
PRIORITY APPLICATION NUMBER: US 60/127,198
PRIORITY FILING DATE: 1999-03-31
PRIORITY APPLICATION NUMBER: US 60/169,162
PRIORITY FILING DATE: 1999-12-06
PRIORITY APPLICATION NUMBER: US 60/177,740
PRIORITY FILING DATE: 2000-01-21
PRIORITY APPLICATION NUMBER: US 60/177,739
PRIORITY FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 382
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: wheat thioredoxin h cDNA
US-10-091-841-3

```

Alignment Scores:	
Pred. No.:	2,956-48
Score:	388.00
Percent Similarity:	82.46%
Best Local Similarity:	56.14%
Query Match:	62.78%
DB:	12
Length:	382
Matches:	64
Conservative:	30
Mismatches:	20
Indels:	0
Gaps:	0

US-09-786-715-8 (1-123) x US-10-091-841-3 (1-382)

QY 2 AAlaGluValGluGluGluValGluValIleGluValIleHisThrMetAlaAspGluTyrPheLeuGln 21
 Dd 37 GCGGCGGTATGGGGGCGGGGAGGTGATCTCCGCTCCACACGCTGGAGCAATGGACCATCAG 96
 QY 22 LeuGlnAsnAlaLysAspSerLysLysLeuIleValValAlaAspMetHisAlaSerTyrCys 41
 Dd 97 ATCCGAGAGGCGCAACCCGCCGCCAAGAAGCGTGGTGATGTGACTTCACAGCATCTCATGTGTC 156

OY	42	GlyProCysArgPheMetIaIaProValLeuAlaGluIleIaLysIysThrProGluLeu	61
Db	157	GGACCAATGCCCGCATTTGTGGCTCCAAATTTCGTGCATTCGCCAAGAAGTCCCAGTGCT	216
OY	62	IlaPheLeuLysValAspValAspGluValaIaCpProValaIaGluGluTySerIleGlu	81
Db	217	GTTTTCTCATAGSTGCAGCTGTATGAACrGAAGACCcATTCTGCAGCAATTACGGTGGAG	276
OY	82	AlaMetProThrPheLeuPheLeuLysAspGlyIuIleValAspLysValaIeGlyIa	101
Db	277	GCCATGCCAACCTTCCTGTTCATCAAGAAGAAGATGTCAAGGACAGGAGGTTGTGGAGCT	336
OY	102	SerLysAspAspLeuGlInalathrIleIaLysHisAlaSer	115
Db	337	ATCAAGAGGAGACTGCACGCACAAGGTGGGCTTACACGGCGCC	378

RESULT 14

```

US-09-938-842A-164
: Sequence 164, Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kreps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF
: TITLE OF INVENTION: SAME, AND METHODS OF USE
: FILE REFERENCE: SCRIP300-3
: CURRENT APPLICATION NUMBER: US/09/938,842A
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227,866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 164
: LENGTH: 360
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-164

```

Alignment Scores:	
Pred. No.:	3,52e-47
Score:	380.50
Percent Similarity:	76.72%
Best Local Similarity:	61.21%
Query Match:	61.57%
DB:	10
length:	366
Matches:	71
Conservative:	18
Mismatches:	26
Indels:	1
Gaps:	1

US-09-786-715-8 (1-123) x US-09-938-842A-164 (1-360)

[illegible]

OY 104 AspAspLeuGlnAlaThrIleAlaIlyshIsAlaSerAlaValAla 119
Db 310 GAAGATCTTACAGCGCAAAATAGTGAACATCTGCTTACAACTGCG 357

RESULT 15

US-10-349-782-9
; Sequence 9, Application US/10349782
; Publication No. US20030143618A1
; GENERAL INFORMATION:
; APPLICANT: Yves Hatzfied
; APPLICANT: Valerie Marie-No. US20030143618A1lle Frankard
; APPLICANT: Anne-Marie Droual
; TITLE OF INVENTION: Method for easy cloning and selection of chimeric DNA molecules
; FILE REFERENCE: 1187-15
; CURRENT APPLICATION NUMBER: US/10/349,782
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: EP 02075373.7
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 659
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thioredoxin of Oryza sativa in vector pDONR201
US-10-349-782-9

Alignment Scores:

Pred. No.:	2.82e-46	Length:	659
Score:	377.00	Matches:	74
Percent Similarity:	78.15%	Conservative:	19
Best Local Similarity:	62.18%	Mismatches:	26
Query Match:	61.00%	Indels:	1
DB:	12	Gaps:	0

US-09-786-715-8 (1-123) x US-10-349-782-9 (1-659)

OY 5 GluGluGlyGlnValIleGlyValHisThrValAspGluTrpLysLeuGlnLeuGlnAsn 24
Db 139 GAGGAGGAGAGTGTGATCGCTGCCACCAAGAGAGTTCGACGCCAGATGACCAAG 198
OY 25 AlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCys 44
Db 199 GCCAAGGAGGCCGCAAGAGTGTGATTAATGACTTCACTGCTCTGCTGCTGCTGCTGC 258
OY 45 ArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGluLeuIlePheLeu 64
Db 259 CGCTTCATCGCCCGCAGTGTGCTGCAATACCCCAAAAAGTCCCTGCTGCTCTCTCCTG 318
OY 65 LysValAspValAspGluValArgProValAlaGluGluTrpSerIleGluAlaMetPro 84
Db 319 AAGGTGTATGTGATGAGCTGAAGAGAGTCTGAAGAGTCAATGTCAGAGCAATGCCG 378
OY 85 ThrPheLeuPheLeuLysAspGlyGluIleValAspLysValValGlyAlaSerLysAsp 104
Db 379 ACCCTCTATT-ATCAAGAGAGTGTGAGGCTGACAGAGTGTGGCCGAGGAGAGAT 437
OY 105 AspLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAlaLaserSerSer 123
Db 438 GACCTCCAGAACACATCGTGAACACAGTGGTGCACCTGCTGCTGCTGCTGCTGCC 494

Search completed: August 17, 2003, 23:43:55
Job time : 146.373 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 19:20:27 ; Search time 1663.43 Seconds
(without alignments)
1797.162 Million cell updates/sec

Title: US-09-786-715-8
Perfect score: 618
Sequence: 1 MAVEEGYGVYGVHTVDEMKL.....DDLQATIAKASAVAAASS 123

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL-frame-p2n.model -DEV-xlp
-Q/cg2_1/USPTO.spool/US09786715/runat_11082003_150514_6048/app-query.fasta.1.1052
-DB-EST -OPMT-fastap -SUFFIX-first -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=ptc -NORM-ext -HEASize=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09786715.ecen_1_1_783_etrunat_11082003_150514_6048 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-FAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST :
1: em_estbda :
2: em_esthmu :
3: em_estlin :
4: em_estmu :
5: em_estrov :
6: em_estropl :
7: em_estro :
8: em_hic :
9: gb_estl :
10: gb_estl2 :
11: gb_hic :
12: gb_est3 :
13: gb_est4 :
14: gb_est5 :
15: em_estfun :
16: em_estom :
17: em_gss_hum :
18: em_gss_inv :
19: em_gss_pin :
20: em_gss_vrt :
21: em_gss_fun :
22: em_gss_mam :
23: em_gss_mus :
24: em_gss_pro :
25: em_gss_rod :
26: em_gss_png :
27: em_gss_vr1 :
28: gb_gss1 :

29: gb_gss2 :*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	618	100.0	441	9	AM705063
2	618	100.0	452	10	BE807885
3	618	100.0	455	10	BE473545
4	618	100.0	464	10	BG238189
5	618	100.0	465	9	AM781479
6	618	100.0	475	10	BE347100
7	618	100.0	479	10	BE807019
8	618	100.0	505	10	BG725950
9	618	100.0	508	10	BE607957
10	618	100.0	510	9	AM568753
11	618	100.0	517	9	AM164347
12	618	100.0	527	12	BM884981
13	618	100.0	532	14	CD414498
14	618	100.0	544	10	BE440397
15	618	100.0	569	12	BM177477
16	618	100.0	577	14	CD414001
17	618	100.0	578	14	CD403924
18	618	100.0	584	14	CD406706
19	618	100.0	608	14	CA935518
20	618	100.0	662	13	BU548381
21	614	99.4	519	14	CA937099
22	613	99.2	360	14	CD416637
23	605	97.9	487	9	A1736736
24	600	97.1	497	12	B1941622
25	595	96.3	425	13	BU763193
26	593	96.0	488	9	AM277335
27	576	93.2	372	9	AM597424
28	572	92.6	511	14	CD407444
29	565	91.4	428	10	BG046853
30	538	87.1	349	10	BF068694
31	535	86.6	426	14	CD416748
32	516	83.5	479	12	BG838458
33	516	83.5	534	14	CA799061
34	516	83.5	616	14	CD410224
35	515	83.3	390	9	A1441505
36	515	83.3	547	9	AM349509
37	515	83.3	556	12	B1471125
38	515	83.3	570	14	CD398312
39	515	83.3	612	14	CD487665
40	511	82.7	373	10	BE210731
41	508	82.2	433	13	BO786368
42	471	76.2	350	9	A1461254
43	452	73.1	464	9	AL386021
44	452	73.1	471	9	AM329521
45	452	73.1	478	9	AL384324

ALIGNMENTS

RESULT 1
AM705063
LOCUS
DEFINITION
sk57b09.y1 Gm-cl019 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl019-6642 5' similar to SW:THIL_TOBAC 007090 THIOREDOXIN H-TYPE 2 ; mRNA sequence.
ACCESSION
AM705063
VERSION
AM705063.1 GI:7569286
KEYWORDS
SOURCE
ORGANISM
EST.
glycine max (soybean)
glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
euroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.				
1 (bases 1 to 441)				
Shoemaker R., Keim, P., Voklin, L., Eppelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harey, N., Schurk, R., Ritter, E., Kohn, S., Ship, T., Jackson, Y., Cardenas, M., McCann, R., Waterson, R. and Wilson, R.				
Public Soybean EST Project				
Unpublished				
Contact: Shoemaker R/Public Soybean EST Project				

FEATURES

Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cu@resgen.com
Insert Length: 657 Std Error: 0.00
Seq Primer: -40RP from GlDco
High quality sequence stop: 425.
Location/Qualifiers

```

source
1. .441
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl019-6642"
/tissue_type="Immature seed coats of greenhouse grown plants"
/lab_host="DH10B (Gibco BRU)"
/clone_id="Gm-cl019"
/vector="pSPORt1 (Life Technologies); Site 1: Not I; Site 2: Sal I; This cDNA library was constructed from mRNA isolated from immature seed coats (200-300 mgs) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restriction site. Sal I linker adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I-Sal I restriction site of the pSPORt1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells (Gibco BRU). This library was constructed by Dr. Lila Vodka and Dr. Anu Khanna."
118 a 88 c 112 g 123 t

```

Alignment Scores:	
pred. No.:	3,31e-75
Score:	618.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
BB:	9
Length:	441
Matches:	123
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-786-715-8 (1-123) x AW705063 (1-441)

QY 1 MetAlaGlUValGluGluGluGlnValIleGlyValHisThrValAspGluTrpLysLeu 20

Db 27 ATGGCTGAATGTGGAAGAGGACAGCTCATGCGCTCCACACCTTGATGATGGAAGCTG 86

QY 21 GlnLeuGlnAsnAlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrp 40

Db 87 CAACTCCAGATGCAGAAAGACTCCAAAAAAGCTGATTGTGGTGGAATTTTACGCTTCCTCG 146

QY 41 CysGlyProCysArgPheMetAlaProValLeuAlaGluIleAlaLysThrProGlu 60

Db 147 TGTGGTCCATGCCGTTTATATGGCCCCAGCTTCTGCACAGATGTGCAAGAAAGAAATCCCTGAA 206

QY	Db	QY	Db
61	LeuIIIPheLeuLysValAspValAspGluValArgProValAlaGluGluLysSerIle	101	AlaSerLysAspAspLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaIleAla
207	TTTATCTTCTCAAAAGTGGATGTGGATGAAGTGAAGGCTGTTCCTGAGGAAATATTCATT	327	GCTAGAGAGAGATACCTTCAGGCACCAATAGCCAAAGCATCATCTGCTGTTCGTGCT
81	GluAlaMetProThrPheLeuPheLeuLysAspGlyGluIleValAspLysValValGly	121	SetSerSer 123
267	GAGGCCATGGCAACCTTCCTCTTGAAGAGTGGGAGATCGGAGCAAGGTGTGGT	387	TCTTCTTCT 395

RESULT	2
BEB07885	
LOCUS	BEB07885
DEFINITION	ss3le05.y1 Gm-cl061 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl061-345 5' similar to SW:TIII_TOBAC Q07090 THIOREDOXIN H-TYPE 2 ; mRNA sequence.
ACCESSTION	BEB07885
VERSION	BEB07885.1 GI:10238997
KEYWORDS	EST.
SOURCE	Glycine max (soybean)
ORGANISM	Glycine max

REFERENCE
AUTHORS
I (phases I to 452)
Shoemaker, R., Keim, P., Vodkin, L., Erpeldding, J., Corvelli, V., Khanna,
A., Bolla, B., Mattira, M., Hillier, L., Kucana, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Stepleco, M., Thelising, B., Allen, M., Bowers
Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
R., Waterston, R. and Wilson, R.
TITLE
Public Soybean EST Project
JOURNAL
Unpublished
COMMENT
Contact: Shoemaker R/Public Soybean EST Project
D. C. 60608-7099

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewartson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp., 2130
South Memorial Parkway Huntville, AL 35801 for further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence shop: 414.
Call: 414-223-1100

```

FEATURES
source
    location/Qualifiers
    1..452
    /organism="Glycine max"
    /mol_type="mrna"
    /db_xref="taxon:3847"
    /clone="GENOME SYSTEMS CLONE ID: Gm-c1061-345"
    /issue_type="mature flowers of field grown plants"
    /lab_host="DH10B"
    /clone_lib="Gm-c1061"
    /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from mature flowers of field grown plants for the cultivar
Raiden. Complementary DNA was synthesized from mRNA using
a primer consisting of a poly(dT) sequence with a XhoI
restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
BASE COUNT
    123 a
    87 c
    115 g
    127 t

```

ORIGIN

Alignment Scores:

Pred. No.: 3,43e-75 Length: 452
 Score: 618.00 Matches: 123
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-786-715-8 (1-123) x BE807885 (1-452)

QY 1 MetAlaGluValGluGluGluGluValIleGlyValHisThrValAspGluTrpLysLeu 20
 |||||||
 Db 21 ATGGCTGAAGTGAAGAAGGACAGCTCATCGCGTCCACACCTTGATGATGAGACTG 80
 |||||||
 QY 21 GlnLeuGlnAsnAlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrp 40
 |||||||
 Db 81 CAACCTCAGAAATCAAAAGACTCCAAAACATGATGTGTGATTTTACTGCTCTCTG 140
 |||||||
 QY 41 CysGlyProCysArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGlu 60
 |||||||
 Db 141 TGTGGTCCAGCCGCTTTTATGCGCCAGTTCTTGCAAGATTCAGAAAGAACTCCTGAA 200
 |||||||
 QY 61 LeuIlePheLeuLysValAspValAspGluValArgProValAlaGluGluTrpSerIle 80
 |||||||
 Db 201 TTGATCTTCTCAAAATGATGATGTGATGAGTCAAGCGCTTCTCTGAGAAATATTCATT 260
 |||||||
 QY 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyGluIleValAlaLysLysValAlaGly 100
 |||||||
 Db 261 GAGGCCATGCGCAACCTTCTCTCTTGAAGATGCGAGATCTGAGCAAGTGTGTGTGT 320
 |||||||
 QY 101 AlaSerLysAspLysLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAla 120
 |||||||
 Db 321 GCTAGTAAGATGATCCTTCAAGCCACCATGACCAACATGATCTGCTGTGCTGCT 380
 |||||||
 QY 121 SerSerSer 123
 |||||||
 Db 381 TCTTCTTCT 389

RESULT 3 BE473545 455 bp mRNA linear EST 04-DEC-2001
 LOCUS BE473545
 DEFINITION sp52d10.y1 Gm-c1043 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1043-1868 5' similar to SW:TH11_TOBAC Q07090 THIOREDOXIN H-TYPE 2 ; mRNA sequence.

ACCESSION BE473545
 VERSION BE473545.1 GI:9564036
 KEYWORDS EST.
 SOURCE glycine max (soybean)
 ORGANISM Glycine max

REFERENCE 1 (bases 1 to 455)
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corryell,V., Khana
 A., Bolla,B., Matra,M., Hillier,L., Kucada,T., Martin,J., Beck,C.,
 Wille,T., Underwood,R., Steptoe,M., Theising,B., Allen,M., Bowers
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuk
 R., Rilter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
 R., Waterston,R. and Wilson,R.
 TITLE Public Soybean EST Project
 JOURNAL unpublished
 COMMENT Contact: Shoemaker R./Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact via email: ccu@resgen.com
 Insert length: 596 Std Error: 0.00
 High quality sequence stop: 444.
 Location/Qualifiers

FEATURES

source

1..455

/organism="Glycine max"

/mol_type="mRNA"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1043-1868"

/tissue_type="Hypocotyl and Plumule, germinating seeds"

/lab_host="DH10B"

/clone_11b="Gm-c1043"

/note="Vector: pT73Pac (Pharmacia). Site 1: EcoRI;
 Site 2: NotI. This cDNA library was constructed from mRNA
 isolated from hypocotyl and plumule tissues of seeds
 germinated for three days of the cultivar Williams.
 Complementary DNA was synthesized from mRNA using a primer
 consisting of a poly(dT) sequence with a NotI restriction
 site. EcoRI adapters were ligated to the blunt-ended cDNA
 fragments followed by digestion with EcoRI and NotI. The
 cDNA fragments were directionally cloned into the
 EcoRI-NotI restriction site of the pT73-Pac vector. The
 ligated cDNA fragments were transformed into DH10B host
 cells (Gibco BRL). This library was constructed by Dr.
 Randy Shoemaker."

BASE COUNT 125 a 89 c 115 g 125 t 1 others
 ORIGIN

Alignment Scores:

Pred. No.: 3,46e-75 Length: 455
 Score: 618.00 Matches: 123
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-786-715-8 (1-123) x BE473545 (1-455)

QY 1 MetAlaGluValGluGluGluGluValIleGlyValHisThrValAspGluTrpLysLeu 20
 |||||||
 Db 34 ATGGCTGAAGTGAAGAAGGACAGCTCATCGCGTCCACACCTTGATGATGAGACTG 93
 |||||||
 QY 21 GlnLeuGlnAsnAlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrp 40
 |||||||
 Db 94 CAACCTCAGAAATCAAAAGACTCCAAAACATGATGTGTGATTTTACTGCTCTCTG 153
 |||||||
 QY 41 CysGlyProCysArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGlu 60
 |||||||
 Db 154 TGTGGTCCAGCCGCTTTTATGCGCCAGTTCTTGCAAGATTCAGAAAGAACTCCTGAA 213
 |||||||
 QY 61 LeuIlePheLeuLysValAspValAspGluValArgProValAlaGluGluTrpSerIle 80
 |||||||
 Db 214 TTGATCTTCTCAAAATGATGATGTGATGAGTCAAGCGCTTCTCTGAGAAATATTCATT 273
 |||||||
 QY 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyGluIleValAlaLysLysValAlaGly 100
 |||||||
 Db 274 GAGGCCATGCGCAACCTTCTCTCTTGAAGATGCGAGATCTGAGCAAGTGTGTGTGT 333
 |||||||
 QY 101 AlaSerLysAspLysLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAla 120
 |||||||
 Db 334 GCTAGTAAGATGATCCTTCAAGCCACCATGACCAACATGATCTGCTGTGCTGCTG 393
 |||||||
 QY 121 SerSerSer 123
 |||||||
 Db 394 TCTTCTTCT 402

RESULT 4 BG238189 464 bp mRNA linear EST 28-NOV-2001
 LOCUS BG238189
 DEFINITION sab63d03.y1 Gm-c1043 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1043-3990 5' similar to SW:TH11_TOBAC Q07090 THIOREDOXIN H-TYPE 2 ; mRNA sequence.

ACCESSION BG238189

VERSION BG238189.1 GI:12773262
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 464)
 REFERENCE Shoemaker,R., Kelm,P., Vodkin,L., Expelting,J., Corvett,V., Khanna
 A., Bolla,B., Marr,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
 R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
 R., Waterston,R. and Wilson,R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Hunttsville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: coueresgen.com
 High quality sequence stop: 463.
 Location/Qualifiers
 1..464
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl043-3990"
 /tissue_type="Hypocotyl and Plumule, germinating seeds"
 /lab_host="DH10B"
 /clone_lib="Gm-cl043"
 /note="Vector: pRT3pac (Pharmacia); Site_1: EcoRI;
 Site_2: NotI; This cDNA library was constructed from mRNA
 isolated from hypocotyl and plumule tissues of seeds
 germinated for three days of the cultivar Williams.
 Complementary DNA was synthesized from mRNA using a primer
 consisting of a poly(dT) sequence with a NotI restriction
 site. EcoRI adapters were ligated to the blunt-ended cDNA
 fragments followed by digestion with EcoRI and NotI. The
 cDNA fragments were directionally cloned into the
 EcoRI-NotI restriction site of the pRT3-pac vector. The
 ligated cDNA fragments were transformed into DH10B host
 cells (Gibco BRL). This library was constructed by Dr.
 Randy Shoemaker."
 BASE COUNT 116 a 100 c 114 g 134 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.55e-75 Length: 464
 Score: 618.00 Matches: 123
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-09-786-715-8 (1-123) x BG238189 (1-464)
 Oy 1 MetlaagiValaigiuglGlycineValaHsthrValaSpGLuTriPlysre 20
 Db 66 ATGGCTGAAGTGAAGAGGACAGCTATCGGCGCTCCACCCGTTGATGATGAGAGCTG 125
 Oy 21 GluLeuglnAsnaAlaLysAspSerLysLysLeuileValaValaAspPheThraLaseTrrp 40
 Db 126 CAATCTCCAGATGCAAAAAGACTCAAAAAGACTGATGTGGTGAGATTACTGCTCCGG 185
 Oy 41 CyselgProCysaGpneMetAlaProValleuAlaGluileAlaLysLysThProGlu 60

Db 186 TGTGTCATGACCGCTTTTATGAGCCCACTCTTCGAGAGANTGCAGAAAACCTCTGAA 245
 Oy 61 LeuilePheLeuLysValaLysPValaSpLuValaArgProValaAlaGluGluTyrSerile 80
 Db 246 TTGATCTTCCTCAAAAGTGAATGTGATGATGAAGAGAGCCCTGTTCGAGAGANTATTCATT 305
 Oy 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyGluileValaLysLysValaGly 100
 Db 306 GAGCCATGCCAACCTCTCTCTTCTTGAAGATGCGAGATCGTGCACAGGTGGTGGT 365
 Oy 101 AlaSerLysAspAspLeuGlnAlaHsrThrleAlaLysSHSLaSerAlaValaAlaAla 120
 Db 366 GCTATGATGAAGATGACCTTCAAGCCACATAGCAGCATGATGCTGTGCTCTCTCT 425
 Oy 121 SerSerSer 123
 Db 426 TCTTCTTCT 434
 RESULT 5
 AM781479
 LOCUS
 DEFINITION s179e04.y1 Gm-cl037 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 Gm-cl037-247 5' similar to SW:TH11_TOBAC Q07090 THIOREDOXIN H-TYPE
 2,, mRNA sequence.
 ACCESSION AM781479
 VERSION AM781479.1 GI:7796082
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max (soybean)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 465)
 REFERENCE Shoemaker,R., Kelm,P., Vodkin,L., Expelting,J., Corvett,V., Khanna
 A., Bolla,B., Marr,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
 Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
 R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
 R., Waterston,R. and Wilson,R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Hunttsville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: coueresgen.com
 Insert Length: 705 Std Error: 0.00
 High quality sequence stop: 437.
 Location/Qualifiers
 1..465
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl037-247"
 /tissue_type="Fully expanded leaves of greenhouse grown
 plants"
 /dev_stage="2 week old"
 /lab_host="DH10B"
 /clone_lib="Gm-cl037"
 /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This
 cDNA library was constructed from mRNA isolated from fully
 expanded leaves of greenhouse grown plants that were 2
 weeks old. The library was prepared using the Life
 Technologies pSuperScript cDNA library construction kit.
 Complementary DNA was synthesized from mRNA using a
 poly(dT) sequence with a NotI restriction site. SalI
 linkers adapters were ligated to the blunt-ended cDNA

fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E. coli Electro-Max DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinois at Urbana-Champaign. email: l-vodkin@uiuc.edu"

BASE COUNT 120 a 98 c 113 g 134 t

ORIGIN

Alignment Scores:

Pred. No.:	3,56e-75	Length:	465
Score:	618.00	Matches:	123
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-786-715-8 (1-123) x AM781479 (1-465)

QY 1 MetAlaGluValGluGluGluValIleGlyValHisThrValAspGluTrpLysLeu 20
 DB 53 ATGGCTGAAGTGAAGAGGAGGACAGTCATCGCGCTCCACACCGCTGATGAGGAAGCTG 112
 QY 21 GlnLeuGlnAsnAlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrp 40
 DB 113 CAATCCCAATGCAAAAGACTCCAAAACATGATTTGCTGATTTTACTCTCTCTG 172
 QY 41 CysGlyProCysArgPheMetAlaProValIleuAlaGluIleAlaLysLysThrProGlu 60
 DB 173 TGTGTGTCATGCGCGTTTATGCCCCAGTCTTGACAGATGCAAAAGAACTCTGTGA 232
 QY 61 LeuIlePheLeuLysValAspValAspGluValArgProValAlaGluLysTrpSerIle 80
 DB 233 TTGATCTTCCTCAAGTGTGATGTGATGAGGAGCCCTGCTGAGCAATATTCATT 292
 QY 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyGluIleValAspLysValValGly 100
 DB 293 GAGGCCATGCCAACCTTCTCTTGTGAAGATGGAGATGCTGGACAAAGTGTGTGT 352
 QY 101 AlaSerLysAspAspLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAlaAla 120
 DB 353 GCTACTAAGAGATGACCTTCACGCCACATAGCAAGCATGATGCTGCTGCTGCT 412
 QY 121 SerSerSer 123
 DB 413 TCTTCTCTCT 421

RESULT 6 475 bp mRNA linear EST 04-DEC-2001
 BE347100
 LOCUS sp34710.y1 Gm-cl043 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl043-188 5' similar to SW:TH11_T0BAC 007090 THIOREDOXIN H-TYPE 2; mRNA sequence.

ACCESSION BE347100
 VERSION BE347100.1 GI:9258953
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

REFERENCE 1 (bases 1 to 475)
 AUTHORS Shoemaker R., Keim P., Vodkin L., Eprelding J., Coryell V., Khanna A., Bolla B., Maria M., Hillier L., Kuababa T., Matlin J., Beck C., Wylie T., Underwood K., Steptoe M., Theising B., Allen M., Bowers Y., Person B., Swaller T., Gibbons M., Pape D., Harvey N., Schurk R., Ritter E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann R., Waterston R. and Willson R.

TITLE Public Soybean EST Project
 JOURNAL Unpublished
 COMMENT Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp, 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: coud@resgen.com
 Insert Length: 906 Std Error: 0.00
 High quality sequence stop: 475.
 Location/Qualifiers

FEATURES
 source 1..475
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl043-188"
 /tissue_type="Hypocotyl and Plumule, germinating seeds"
 /lab_host="DH10B"
 /clone_11b="Gm-cl043"
 /note="vector: pTV73pac (Pharmacia); Site_1: EcoRI; Site_2: NotI; This cDNA library was constructed from mRNA isolated from hypocotyl and plumule tissues of seeds germinated for three days of the cultivar Williams. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and NotI. The cDNA fragments were directionally cloned into the EcoRI-NotI restriction site of the pTV73-pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

BASE COUNT 126 a 97 c 118 g 134 t

ORIGIN

Alignment Scores:

Pred. No.:	3.67e-75	Length:	475
Score:	618.00	Matches:	123
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-786-715-8 (1-123) x BE347100 (1-475)

QY 1 MetAlaGluValGluGluGluValIleGlyValHisThrValAspGluTrpLysLeu 20
 DB 44 ATGGCTGAAGTGAAGAGGAGGACAGTCATCGCGCTCCACACCGCTGATGAGGAAGCTG 103
 QY 21 GlnLeuGlnAsnAlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrp 40
 DB 104 CAATCCCAATGCAAAAGACTCCAAAACATGATTTGCTGATTTTACTCTCTCTG 163
 QY 41 CysGlyProCysArgPheMetAlaProValIleuAlaGluIleAlaLysLysThrProGlu 60
 DB 164 TGTGTGTCATGCGCGTTTATGCCCCAGTCTTGACAGATGCAAAAGAACTCTGTGA 223
 QY 61 LeuIlePheLeuLysValAspValAspGluValArgProValAlaGluLysTrpSerIle 80
 DB 224 TTGATCTTCCTCAAGTGTGATGTGATGAGGAGCCCTGCTGAGCAATATTCATT 283
 QY 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyGluIleValAspLysValValGly 100
 DB 284 GAGGCCATGCCAACCTTCTCTTGTGAAGATGGAGATGCTGGACAAAGTGTGTGT 343
 QY 101 AlaSerLysAspAspLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAlaAla 120
 DB 344 GCTACTAAGAGATGACCTTCACGCCACATAGCAAGCATGATGCTGCTGCTGCT 403
 QY 121 SerSerSer 123
 DB 404 TCTTCTCTCT 412

RESULT 7
BE807019
LOCUS 479 bp mRNA linear EST 06-DEC-2001
DEFINITION ss10e10.y1 Gm-cl047 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl047-2563 5' similar to SW:TH11.TOBAC 007090 THIREDOXIN H-TYPE 2 ; , mRNA sequence.
ACCESSION BE807019
VERSION BE807019.1 GI:10238131
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 479)
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE Public Soybean EST Project
JOURNAL Unpublished
COMMENT Contact: Shoemaker R./Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
 High quality sequence stop: 449.
FEATURES
 source
 1..479
 Location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl047-2563"
 /tissue_type="Immature leaves (unfurling trifoliolate) of greenhouse grown plants"
 /dev_stage="2 week old"
 /lab_host="DH10B"
 /clone_lib="Gm-cl047"
 /note="Vector: pSPORT1; Site1: NotI; Site2: SalI. This cDNA library was constructed from mRNA isolated from Immature leaves (unfurling trifoliolate) of greenhouse grown plants that were 2 week old. The library was prepared using the Life Technologies superscript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restriction site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinois at Urbana-Champaign (email 1-vodkin@uiuc.edu)"

US-09-786-715-8 (1-123) x BE807019 (1-479)
OY 1 MetLaIGuValaIGuIGuValaIlleGlyValaHstHrrValaSpGuTrpLysLeu 20
Db 18 ATGGCTGAAGTGAAGAGGAGGACAGCTTCGCGCTCCACACCGTTGATGATGAGAGCTG 77
OY 21 GlnLeuGlnAsnaAlaLysAspSerLysLysLeuIleValaValaAspPheThaLysSerTrp 40
Db 78 CAACTCCAGATGCAAAAAGACTCAAAAACATGATTTGGTGGATTTTACGCTTCCTGG 137
OY 41 CysGlyProCysArGpHeMetAlaProValLeuAlaGluIleAlaLysLysThProGlu 60
Db 138 TGTGCTCAGTCGCTTTATGCGCCCGCTTCCTTCAGAGATGCAAGAAACCTCGAA 197
OY 61 LeuIlePheLeuLysValaSpValaAspGluValaLrProValaAlaGluIGuTrpSerIle 80
Db 198 TTGATCTTCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 257
OY 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyLuuIleValaAspLysValaGly 100
Db 258 GAGGCCATGCCACCTTCCTCTTCTTGAACATGCGCAGATCGTGACAGTGCTGTGCT 317
OY 101 AlaserLysAspAspLeuGlnAlaThrIleAlaLysHisAlaSerAlaValaAlaAla 120
Db 318 GCTAGTAAGATGACCTTCAAGCCACCATAGCCAAAGATGATCTGCTGTGCTGCT 377
OY 121 SerSerSer 123
Db 378 TCTTCTTCT 386
RESULT 8
BG725950
LOCUS 505 bp mRNA linear EST 29-NOV-2001
DEFINITION ssel1004.y1 Gm-cl067 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl067-2383 5' similar to SW:TH11.TOBAC 007090 THIREDOXIN H-TYPE 2 ; , mRNA sequence.
ACCESSION BG725950
VERSION BG725950.1 GI:14011028
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 505)
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE Public Soybean EST Project
JOURNAL Unpublished
COMMENT Contact: Shoemaker R./Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
 High quality sequence stop: 419.
FEATURES
 source
 1..505
 Location/Qualifiers
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl067-2383"
 /tissue_type="Germinating shoot, 3 day old seedling, auxin

treatment"
/lab_host="DH10B"
/clone_lib="Gm-cl067"
/note="Vector: pBluescript II SK-; Site.1: EcoRI; Site.2: XhoI; The cDNA library was constructed from mRNA isolated from germinating shoots of 3 day old seedling for the cultivar Williams 82. The seedlings were germinated in a growth chamber using germination paper in a solution containing 100ppm auxin. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 141 a 91 c 128 g 145 t

ORIGIN

Alignment Scores:
Pred. No.: 3,99e-75 Length: 505
Score: 618.00 Matches: 123
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-786-715-8 (1-123) x BG725950 (1-505)

QY 1 MetAlaGluValGluGluGluGluValIleGlyValHisThrValAspGluTrpLysLeu 20
DB 11 ATGGCTGAAGTGGAGAGGAGACAGTCATCGGCTCACACCGTTATGATGATGAGAGCTG 70
QY 21 GlnLeuGlnAsnAlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrp 40
DB 71 CAACCTCAGATGCAAAAGACTCCAAAAAAGTATGATGATGATTTACTGCTCTCTGG 130
QY 41 CysGlyProCysArgPheMetAlaProValLeuAlaGluIleAlaLysThrProGlu 60
DB 131 TGTGGTGCATGCGCGTTTATGCGCCAGTCTTGACAGATTGCAAGAAAGAACTCTCGAA 190
QY 61 LeuIlePheLeuLysValAspValAspGluValArgProValAlaGluGluTrpSerIle 80
DB 191 TTGATCTCTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
QY 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyGluIleValAspLysValAlaGly 100
DB 251 GAGGCCATGCAACCTCTCTCTGAAAGATGCGAGATGCTGGAACAAGTGGTGGT 310
QY 101 AlaSerLysAspLysLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAla 120
DB 311 GCTAGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 370
QY 121 SerSerSer 123
DB 371 TCTTCTTCT 379

RESULT 9
BE607957 508 bp mRNA linear EST 04-DEC-2001
LOCUS BE607957
DEFINITION sq19b02.y1 Gm-cl046 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl046-1252.5'. similar to SW:TH11_T0BAC Q07090 THIOREDOXIN H-TYPE 2'; mRNA sequence.

ACCESSION BE607957
VERSION BE607957.1 GI:9898989
KEYWORDS EST.
SOURCE glycine max (soybean)
ORGANISM glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 508)
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpellding, J., Corvett, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Treisman, B., Allen, M., Bowers, Y., Person, B., Smaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE Public Soybean EST Project
JOURNAL Unpublished
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact via email: cou@resgen.com
Insert Length: 731 Std Error: 0.00
High quality sequence stop: 476.
Location/Qualifiers
1. 508
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl046-1252"
/tissue="Germinating Seeds"
/lab_host="DH10B"
/clone_lib="Gm-cl046"
/note="Vector: PT73Pac (Pharmacia); Site.1: EcoRI; Site.2: NotI; This cDNA library was constructed from mRNA isolated from seeds germinated for three days of the cultivar Williams. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestions with EcoRI and NotI. The cDNA fragments were directionally cloned into the EcoRI-NotI restriction site of the PT73-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

BASE COUNT 140 a 93 c 128 g 147 t

ORIGIN

Alignment Scores:
Pred. No.: 4.02e-75 Length: 508
Score: 618.00 Matches: 123
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-786-715-8 (1-123) x BE607957 (1-508)

QY 1 MetAlaGluValGluGluGluGluValIleGlyValHisThrValAspGluTrpLysLeu 20
DB 1 ATGGCTGAAGTGGAGAGGAGACAGTCATCGGCTCACACCGTTATGATGATGAGAGCTG 60
QY 21 GlnLeuGlnAsnAlaLysAspSerLysLysLeuIleValValAspPheThrAlaSerTrp 40
DB 61 CAACCTCAGATGCAAAAGACTCCAAAAAAGTATGATGATGATTTACTGCTCTCTGG 120
QY 41 CysGlyProCysArgPheMetAlaProValLeuAlaGluIleAlaLysThrProGlu 60
DB 121 TGTGGTGCATGCGCGTTTATGCGCCAGTCTTGACAGATGCAAGAAAGAACTCTGAA 180
QY 61 LeuIlePheLeuLysValAspValAspGluValArgProValAlaGluGluTrpSerIle 80
DB 181 TTGATCTCTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyGluIleValAspLysValAlaGly 100

AUTHORS
 Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Corryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Smaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Riter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE
 Public Soybean EST Project

JOURNAL
 Unpublished

COMMENT
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact via email: c@eresgen.com
 Insert Length: 782 Std Error: 0.00
 High quality sequence stop: 417.

FEATURES
 Location/Qualifiers
 1..517
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl023-141"
 /tissue_type="seed coats of greenhouse grown plants"
 /lab_host="DH10B"
 /clone_lib="Gm-cl023"
 /note="Vector: pSPORT1; Site-1: SalI; Site-2: NotI; This cDNA library was constructed from mRNA isolated from seed coats (100-200mgs) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restriction site. Sal I linkers adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I-Sal I restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."

BASE COUNT
 140 a 96 c 129 g 152 t

ORIGIN

Alignment Scores:
 Pred. No.: 4.12e-75 Length: 517
 Score: 618.00 Matches: 123
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-786-715-8 (1-123) x AW164347 (1-517)

QY 1 Metatagluvalglunglglglnvalilleglyvalhlsfhrvalasplutrrplysleu 20
 |||||||
 DB 27 ATGGCTGAAGTGAAGAGGACGACGCGGCGCCACACCGCTGATGAGGAAGCTG 86
 |||||||
 QY 21 Glnleuglnasnalylaspsersylsleuilevalvalasphetheralasertp 40
 |||||||
 DB 87 CAACGCCAGATGCCAAAGACCTCCAAAACATGATTTGGTGATTTTACTGCTTCTG 146
 |||||||
 QY 41 Cysgilyprocyasrphemeretalaprovalleualagluilealalsylslythrproglu 60
 |||||||
 DB 147 TGTGTCATGCGCGTTTATGCGCCCGAGTTCTTGACAGATGCAAGAAACCTCTGAA 206
 |||||||
 QY 61 leuilepbeleulyvalasplvalasplvalasplvalasplvalasplvalaspl 80
 |||||||
 DB 207 TTGATCTTCTCCTCAAGTGGATGTGATGAAGGAGCGCTGAGGAAATATTCATT 266
 |||||||
 QY 81 Gualamelprothrphleupheleulyaspsglyluilevalasplvalasplval 100

DB 267 GAGGCATGCCAACCTTCTCTTCTGAAAGAGGAGATGCTGGACAAAGTGCTGT 326
 |||||||

QY 101 AlaSerlyaspspleuglnalharhilealalyshisAlaSerAlaValAlaAla 120
 |||||||

DB 327 GCTAGTAAGGATGACCTTCAGACCATAGCAAGCATGCTGCTGCTGCT 386
 |||||||

QY 121 SerSerSer 123
 |||||||

DB 387 TCTTCTTCT 395

RESULT 12
 BM884981
 LOCUS
 DEFINITION
 527 bp mRNA linear EST 08-MAR-2002
 sal93d11.y1 Gm-cl063 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-cl063-3622 5' similar to SW:TH1170BAC 007090 THIOREDOXIN H-TYPE 2', mRNA sequence.

ACCESSION
 BM884981
 VERSION
 KEYWORDS
 EST.

SOURCE
 ORGANISM
 Glycine max (soybean)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE
 1 (bases 1 to 527)
 Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Corryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Smaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Riter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE
 Public Soybean EST Project

JOURNAL
 Unpublished

COMMENT
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact: c@eresgen.com web site: www.resgen.com
 Seq primer: -40RP from Gibco
 High quality sequence stop: 421.

FEATURES
 Location/Qualifiers
 1..527
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-cl063-3622"
 /tissue_type="Germinating shoot, 24 hour germination"
 /lab_host="DH10B"
 /clone_lib="Gm-cl063"
 /note="Vector: pBluescript II SK+; Site-1: EcoRI; Site-2: XhoI; The cDNA library was constructed from mRNA isolated from germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to harvesting the germinating shoots. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."

BASE COUNT
 144 a 98 c 130 g 155 t

ORIGIN

Alignment Scores:

Pred. No.: 4,236-75 Length: 527
 Score: 618.00 Matches: 123
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-786-715-8 (1-123) x BM884981 (1-527)

QY 1 MetlaagiuvaiIgluIgluIgluValIleclIyValIhsthrValAspGluTrpLysLeu 20
 |||||||
 Db 32 ATGGCTGAAGTGAAGAGGAGGACAGGTCAATCGCGCCACACCGTTGATGAGTGAAGCTG 91
 |||||||
 QY 21 GluLeuGlnAsnAlaLysAspSerLysLysLeuIleValIAspPheThrAlaSerTrp 40
 |||||||
 Db 92 CAATCCAGATGCAAAAGACTCCAAAACACTGATGGTGGATTTACTGCTTCCCTGG 151
 |||||||
 QY 41 CysglIProCysArgPheMetAlaProValLeuAlaIleValIAspLysThrProGlu 60
 |||||||
 Db 152 TGTGGTCCATGCGCTTTATGAGCCCACTTCTTGACAGAGATTGCAAGAAAACCTCCGAA 211
 |||||||
 QY 61 LeuIlePheLeuLysValAspValAspGluValArgProValAlaIleGluTrpSerIle 80
 |||||||
 Db 212 TTGATCTTCCTCAAGTGAAGTGAATGATGAGGCTGTTGCTGAGGAATATTCATT 271
 |||||||
 QY 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyIleValIAspLysValIAspGly 100
 |||||||
 Db 272 GAGGCCATGCCACCTTCTCTTCTTGAAAGATGCCAGATCGTGACAAAGTGTTGCT 331
 |||||||
 QY 101 AlaserLysAspAspLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAla 120
 |||||||
 Db 332 GCTAGTAAGATGACCTTCAAGCCACCATACGATGATGCTGCTGCTGCTGCT 391
 |||||||
 QY 121 SerSerSer 123
 |||||||
 Db 392 TCTTCTTCT 400

RESULT 13

CD414498

LOCUS Gm.c46654 Soybean induced by Salicylic Acid glycine max cDNA 3', 532 bp mRNA linear EST 07-JUN-2003

DEFINITION mRNA sequence.

ACCESSION CD414498.1 GI:31472470

VERSION CD414498

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

REFERENCE Tian A.-G., Wang, J., Cui, P., Han, Y.-J., Xu, H., Cong, L.-J., Huang, X.-G., Wang, X.-L., Jiao, Y.-Z., Wang, B.-J., Wang, Y.-J., Zhang, J.-S., Chen, S.-Y. and Yu, J.

AUTHORS Soybean Expressed Sequence Tags sequencing

COMMENT Unpublished

TITLE Plant Biotechnology Laboratory

JOURNAL Institute of Genetics and Developmental Biology, CAS, China

CONTACT: Chen S.-Y.

DETAILED: 86-10-6486859

TELEPHONE: 86-10-64873428

FAX: Email: sychen@genetics.ac.cn

SYNOPSIS: sychen@genetics.ac.cn

SEGMENT: Seg primer: 17 primer.

LOCATION/Qualifiers

1..532

FEATURES

SOURCE

/organism="Glycine max"

/mol_type="mRNA"

/cultur="Kefeng 1"

/db_xref="taxon:3847"
 /tissue_type="Seedlings"
 /tissue="two-week seedlings"
 /lab_host="Xil-Blue MRF" strain"
 /clone_lib="Soybean induced by Salicylic Acid"
 /note="Vector: pBluescript SK⁺ Site.1: EcoR I; Site.2: Xho I; The cDNA library was constructed by He, C-Y from mRNA isolated from two-week seedlings (cultivar Kefeng 1) treated by spraying 2.0mM salicylic acid for 24, 36, 48 and 72 h. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into Xil-Blue MRF host cells (Stratagene)."

BASE COUNT

ORIGIN

158 a 135 c 94 g 145 t
 Alignment Scores:
 Pred. No.: 4,286-75 Length: 532
 Score: 618.00 Matches: 123
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-09-786-715-8 (1-123) x CD414498 (1-532)

QY 1 MetlaagiuvaiIgluIgluIgluValIleclIyValIhsthrValAspGluTrpLysLeu 20
 |||||||
 Db 511 ATGGCTGAAGTGAAGAGGAGGACAGGTATCGCGCCACACCGTTGATGAGTGAAGCTG 452
 |||||||
 QY 21 GluLeuGlnAsnAlaLysAspSerLysLysLeuIleValIAspPheThrAlaSerTrp 40
 |||||||
 Db 451 CAATCCAGATGCAAAAGACTCCAAAACACTGATGGTGGATTTACTGCTTCCCTGG 392
 |||||||
 QY 41 CysglIProCysArgPheMetAlaProValLeuAlaIleValIAspLysThrProGlu 60
 |||||||
 Db 391 TGTGGTCCATGCGCTTTATGAGCCCACTTCTTGACAGAGATTGCAAGAAAACCTCCGAA 332
 |||||||
 QY 61 LeuIlePheLeuLysValAspValAspGluValArgProValAlaIleGluTrpSerIle 80
 |||||||
 Db 331 TTGATCTTCCTCAAGTGAAGTGAATGATGAGGCTGTTGCTGAGGAATATTCATT 272
 |||||||
 QY 81 GluAlaMetProThrPheLeuPheLeuLysAspGlyIleValIAspLysValIAspGly 100
 |||||||
 Db 271 GAGGCCATGCCACCTTCTCTTCTTGAAAGATGCCAGATCGTGACAAAGTGTTGCT 212
 |||||||
 QY 101 AlaserLysAspAspLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAla 120
 |||||||
 Db 211 GCTAGTAAGATGACCTTCAAGCCACCATACGATGATGCTGCTGCTGCTGCT 152
 |||||||
 QY 121 SerSerSer 123
 |||||||
 Db 151 TCTTCTTCT 143

RESULT 14

BE440397

LOCUS sp45405.y1 Gm-c1043 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1043-1161 5' similar to SW:TH11.TOBAC 007090 THIOREDOXIN H-TYPE 2, mRNA sequence.

DEFINITION

ACCESSION BE440397

VERSION BE440397

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

REFERENCE Tian A.-G., Wang, J., Cui, P., Han, Y.-J., Xu, H., Cong, L.-J., Huang, X.-G., Wang, X.-L., Jiao, Y.-Z., Wang, B.-J., Wang, Y.-J., Zhang, J.-S., Chen, S.-Y. and Yu, J.

AUTHORS Soybean Expressed Sequence Tags sequencing

COMMENT Unpublished

TITLE Plant Biotechnology Laboratory

JOURNAL Institute of Genetics and Developmental Biology, CAS, China

CONTACT: Chen S.-Y.

DETAILED: 86-10-6486859

TELEPHONE: 86-10-64873428

FAX: Email: sychen@genetics.ac.cn

SYNOPSIS: sychen@genetics.ac.cn

SEGMENT: Seg primer: 17 primer.

LOCATION/Qualifiers

1..532

FEATURES

SOURCE

/organism="Glycine max"

/mol_type="mRNA"

/cultur="Kefeng 1"

protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the Bluescript vector. The ligated cDNA fragments were transformed into E. coli Electromax DH10B host cells. Plant care, inoculations, and library construction were performed by Steve Clough (Ulla Vodka lab, University of Illinois).

BASE COUNT 147 a 108 c 135 g 179 t
ORIGIN

Alignment Scores:

Pred. No.:	4.7e-75	Length:	569
Score:	618.00	Matches:	123
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-786-715-8 (1-123) x BM177477 (1-569)

OY	1	MetAlaGluValGluGluGluValGluValHisThrValAspGluTrpLysLeu	20
DB	55	ATGGCTGAAGTGGAAAGGACAGGTCTATCGGCGTCCACACCGTTGATGAGTGAAGCTG	114
OY	21	GlnLeuGlnAsnAlaLysAspSerLysLeuIleValValAspPheThrAlaSerTrp	40
DB	115	CAACTCCAGATGCAAAAGACTCCAAAAGATGTTGGTGGATTACTGCTTCCCTGG	174
OY	41	CysGlyProCysArgPheMetAlaProValLeuAlaGluIleAlaLysLysThrProGlu	60
DB	175	TGTGGTCCATCCCGTTTATGGCCCCAGTCTCTGCAGAGATTGCCAAAGAAAACCTCTGAA	234
OY	61	LeuIlePheLeuLysValAspValAspGluValArgProValAlaGluGluTyrSerIle	80
DB	235	TTGATCTCTCTCAAAAGTGTGATGATGAAGGCTGTGCTGAGGAATATTCATTT	294
OY	81	GluAlaMetProThrPheLeuPheLeuLysAspGluIleValAspLysValValGly	100
DB	295	GAGGCCATGCCAACCTCTCTCTTGAAGATGGCGAGATCGTGACACAGGTGGTGGT	354
OY	101	AlaSerLysAspAspLeuGlnAlaThrIleAlaLysHisAlaSerAlaValAlaAlaAla	120
DB	355	GCTAGTAGAGATGACCTTCAAGCCACCATAGCCAAAGCATGCTGCTGTGCTGCTGCT	414
OY	121	SerSerSer 123	
DB	415	TCTTCTTCT 423	

Search completed: August 17, 2003, 23:34:27
Job time : 1669.43 secs

TITLE cDNA expressed in Ricinus cotyledons
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 603)
AUTHORS Doljener, E.
TITLE Direct Submission
JOURNAL Submitted (04-Apr-1996) Doljener E., University of Bayreuth,
Department of Plant Physiology, Universitaetsstr.30, Bayreuth,
Germany, 95440

FEATURES
source Location/Qualifiers
1..603
/organism="Ricinus communis"
/mol_type="mRNA"
/cultivar="Sanguineus"
/db_xref="taxon:3988"
/clone="PDRH018"
/tissue_type="cotyledon"
/clone_lib="lambda Excel"
/dev_stage="seedling"
23..379
/codon_start=1
/product="thioredoxin"
/protein_id="CAA94534.1"
/db_xref="GI:1259594"
/db_xref="SPTREMBL:Q43636"
/translation="MAEEGVIGCHTVEANNEOLQKNDTKGLIVDFETASWCGPCR
FIAPLAEIAKLKPLPVETFLKVDDELKTVAHEMAVESPTFELKEGKIMDKVGAKK
DELOOTIAKHMATST"

CDS
BASE COUNT 179 a 101 c 157 g 166 t
ORIGIN

Alignment Scores:
Pred. No.: 5.01e-44 Length: 603
Score: 442.00 Matches: 80
Percent Similarity: 87.61% Conservative: 19
Best Local Similarity: 70.80% Mismatches: 14
Query Match: 72.82% Indels: 0
DB: 8 Gaps: 0

US-09-786-715-4 (1-118) x RCHTHIORXN (1-603)

QY 3 SerSerGIUGLUGLIGLIVaIIleGLICySHISserValAspGLUTPrLysGLInphe 22
Db 26 GCAGCAGAGAGAGGCGCAAGTGCATCGGCGCCACACTGTGAGCATGCAATGCAATG 85
QY 23 GlnLysGLIVaIAspSerLysLysLeuValaIIleAspPheThAlaSerTrpLysGLY 42
Db 86 CAGAGGGAATGATACCAAGGACTGATCGTTGTGATTACTGCTTCATGATGAGTGA 145
QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
Db 146 CCATGCCGTTTCATGTCGCCCTTCTGGCTGAGCGGCCAAGAACTGCCAATGTTCAC 205
QY 63 PheLeuLysValAspValAspGLuleuLysThrValaIaGluGluPheLysValaIua 82
Db 206 TTCCGAGAGGAGTGCATGATGACACTGCTGCTCAAGACTGGGCTGTGAGTCA 265
QY 83 MetProThrPheValPheLeuLysGLIUGLIVaIaGluArgLeuValaIaArg 102
Db 266 ATGCCAACCTTATCTCTCGAAGGAGGAGATTAAGACAAAGGCTGTGAGCAAG 325
QY 103 LysGLIUGLIVaIaThrValaIaLysLysGLIaIa 115
Db 326 AAAGCAGAACTGCACCAACTATACGCAACATGCGCT 364

RESULT 14
AF323593 664 bp mRNA linear PLN 02-NOV-2001
LOCUS AF323593
DEFINITION Prunus persica thiodoxin H mRNA, complete cds.
ACCESSION AF323593
VERSION AF323593.1 GI:16588842
KEYWORDS
SOURCE Prunus persica (peach)
ORGANISM Prunus persica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE
AUTHORS Callahan, A.M., Morgens, P.H. and Cohen, R.A.
TITLE Isolation and initial characterization of cDNAs for mRNAs regulated
during peach fruit development
JOURNAL J. Am. Soc. Hortic. Sci. 118, 531-537 (1993)
REFERENCE
AUTHORS Callahan, A.M., Morgens, P.H., Cohen, R.A. and Scorza, R.
TITLE Regulation of peach gene expression in a peach/almond hybrid
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 664)
AUTHORS Callahan, A.M., Dunn, L.L. and Cohen, R.A.
TITLE Direct Submission
JOURNAL Submitted (22-NOV-2000) USDA-ARS, Appalachian Fruit Research
Station, 45 Wiltshire Rd., Kearneysville, WV 25430, USA

FEATURES
source Location/Qualifiers
1..664
/organism="Prunus persica"
/mol_type="mRNA"
/cultivar="B612615"
/db_xref="taxon:3760"
/clone="pch306c"
/tissue_type="ripe fruit"
71..481
/codon_start=1
/product="thioredoxin H"
/protein_id="AAL26915.1"
/db_xref="GI:16588843"
/translation="MAEENOVIGCHTQAMEBOLKHNKNIIVYDFETASWCGPCL
IAPILAEIAKLKPLPVETFLKVDDELKTVAHEMAVESPTFELKEGKIVDKVGAKKD
ELQIVKHHVMAAASATSAATATATATATSA"

CDS
BASE COUNT 182 a 147 c 161 g 174 t
ORIGIN

Alignment Scores:
Pred. No.: 5.19e-43 Length: 664
Score: 434.00 Matches: 81
Percent Similarity: 84.35% Conservative: 16
Best Local Similarity: 70.43% Mismatches: 18
Query Match: 71.50% Indels: 0
DB: 8 Gaps: 0

US-09-786-715-4 (1-118) x AF323593 (1-664)

QY 4 SerGIUGLUGLIGLIVaIIleGLICySHISserValAspGLUTPrLysGLInphe 23
Db 74 GCGAGGAAATCAAGTGCATCGGCGCCACACTCAAGCCTGGGAAGCAGCTCCAT 133
QY 24 LysGLIVaIAspSerLysLysLeuValaIIleAspPheThAlaSerTrpLysGLY 43
Db 134 AAGGGAAGAGAAAGAAAGTGTGGTGGATTCACGCTTCGCTGCTGAGACCG 193
QY 44 CysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIlePhe 63
Db 194 TGCCGCTGATGCCGCCCATCTTGGCGGAGTGGCTAAGAACCCAGAGTACGTTG 253
QY 64 LeuLysValAspValAspGLuleuLysThrValaIaGluGluPheLysValaIuaMet 83
Db 254 CTAAAGGTGAGAGTGCATGATGACACTGCTTCCGAGAGTGGGCTGTGAGCAATG 313
QY 84 ProThrPheValPheLeuLysGLIUGLIVaIaGluArgLeuValaIaArgLys 103
Db 314 CCTACCTTCCTTCTCGAAGGAGGAGATTAAGACAAAGTGTGAGTGCAGAA 373
QY 104 GluGLIVaIaThrValaIaLysLysGLIaIa 118
Db 374 GACGAGTACAGATCAAACTTGCACAGCATGTGCGCGCCGCC 418

RESULT 15
PSA319808 593 bp mRNA linear PLN 17-JUN-2001
LOCUS PSA319808

NTT RNA LOCUS 698 bp MRNA linear PLN 15-FEB-1994
 DEFINITION N. tabacum mRNA for thioredoxin.
 ACCESSION X58527
 VERSION X58527.1 GI:20046
 KEYWORDS thioredoxin.
 SOURCE Nicotiana tabacum (common tobacco)
 ORGANISM Nicotiana tabacum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
 REFERENCE 1 (bases 1 to 698)
 AUTHORS Marty, I. and Meyer, Y.
 TITLE Nucleotide sequence of a cDNA encoding a tobacco thioredoxin
 JOURNAL Plant Mol. Biol. 17 (1), 143-147 (1991)
 MEDLINE 91329721
 PUBMED 1868216
 REFERENCE 2 (bases 1 to 698)
 AUTHORS Brugidou, C., Marty, I., Chartier, Y. and Meyer, Y.
 TITLE The Nicotiana tabacum genome encodes two cytoplasmic thioredoxin genes which are differentially expressed
 JOURNAL Mol. Gen. Genet. 238 (1-2), 285-293 (1993)
 MEDLINE 93241165
 PUBMED 8479434
 REFERENCE 3 (bases 1 to 698)
 AUTHORS Meyer, Y.
 TITLE Direct Submission
 JOURNAL Submitted (14-FEB-1991) Y. Meyer, Laboratoire de Physiologie et Biologie, Moleculaire Vegetale, Universite av de Villeneuve, 66860 Perpignan, France
 COMMENT Gene product is probably cytoplasmic.
 FEATURES
 source location/Qualifiers
 1. 698
 /organism="Nicotiana tabacum"
 /mol_type="mRNA"
 /strain="white Burley"
 /db_xref="taxon:4097"
 /clone_lib="plasmid pTZ19"
 /dev_stage="in vitro cells"
 1. 682
 /evidence=experimental
 79. 459
 /codon_start=1
 /product="thioredoxin"
 /protein_id="CAA41415.1"
 /db_xref="GI:20047"
 /db_xref="SWISS-PROT:P29449"
 /translation="MAANDATSSSEGCVEEMNEFFKGVETKKLVVDFTAS
 WCGPREFIADIAKMPHVLFLVDDELKTVSAEWSVEAMPTEFKDKEVDR
 VVGAKKEELQOTIVKHAAPATVTA"
 polyA_signal 468. 473
 polyA_signal 511. 517
 polyA_site 682
 BASE COUNT 192 a 117 c 164 g 225 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3 44e-49 length: 698
 Score: 485.50 Matches: 90
 Percent Similarity: 89.08% Conservative: 16
 Best Local Similarity: 75.63% Mismatches: 10
 Query Match: 79.98% Indels: 3
 DB: 8 Gaps: 1
 US-09-786-715-4 (1-118) x NTT RNA (1-698)
 QY 3 SerSerGluGluGlyGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
 Db 100 TCATCCGAGAGGAGGAGCAAGTGTGGCTGCCACAGAGTGTGAGGAATGGAACGAGTACTTC 159
 QY 23 GlnLysGlyValAspSerLysLysLeuValValIleAspPheThrLysAspTrpCysGly 42
 Db 160 AAGAAAGGCGTGTGACTAAGAAAGTGTGTGTGCTGCTTACTCTTATGCTGCTGCTGCTGCT 219

QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
 Db 220 CCTTGGCGTTTATFTGCCCAATCTTCTGCGATCTGTAGAAAGATGCCCAATGTTATA 279
 QY 63 PheLeuLysValAspValAspGluLeuLysThrValAlaGluGluPheLysValGluAla 82
 Db 280 TTCCTCAAGGTTGATGTGATGATGAACGACGCTTTCACCGCAATGAGTGTGGAGGCA 339
 QY 83 MetProThrPheValPheLeuLysGluGlyLysGluValGluLysArgLeuValGlyAlaArg 102
 Db 340 ATGCCACATTTTGTCTTCAATTAAGATGGAAGAAAGATGACAGAGTGTGGTGCAGAG 399
 QY 103 LysGluGluLeuGluAlaThrValGluLysHisGlyAla-----IleThrAla 118
 Db 400 AAGAGAGAGTTGCAGACAGACCAATGAGAACATGCTGCTCTACTGCTACTGCT 456
 RESULT 2
 AR016869 653 bp DNA linear PAT 05-DEC-1998
 LOCUS Sequence 103 from patent US 5777200.
 DEFINITION AR016869
 ACCESSION AR016869
 VERSION AR016869.1 GI:3973146
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 653)
 AUTHORS Ryals, J.A., Alexander, D.C., Goodman, R.M. and Stinson, J.R.
 TITLE Chemically regulatable and anti-pathogenic DNA sequences and uses thereof
 JOURNAL Patent: US 5777200-A 103 07-JUL-1998;
 FEATURES location/Qualifiers
 source 1. 653
 /organism="unknown"
 BASE COUNT 165 a 114 c 157 g 215 t 2 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 8 84e-48 length: 653
 Score: 473.50 Matches: 90
 Percent Similarity: 88.33% Conservative: 16
 Best Local Similarity: 75.00% Mismatches: 10
 Query Match: 78.01% Indels: 4
 DB: 6 Gaps: 1
 US-09-786-715-4 (1-118) x AR016869 (1-653)
 QY 3 SerSerGluGluGlyGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
 Db 69 TCATCCGAGAGGAGGAGCAAGTGTGGCTGCCACAGAGTGTGAGGAATGGAACGAGTACTTC 128
 QY 23 GlnLysGlyValAspSerLysLysLeuValValIleAspPheThrLysAspTrpCysGly 42
 Db 129 AAGAAAGGCGTGTGACTAAGAAAGTGTGTGTGCTGCTGCTTACTCTTATGCTGCTGCGS 188
 QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
 Db 189 CCTTGGCGTTTATFTGCCCAATCTTCTGCGATCTGTAGAAAGATGCCCAATGTTATA 248
 QY 63 PheLeuLysValAspValAspGluLeuLysThrValAlaGluGluPheLysValGluAla 82
 Db 249 TTCCTCAAGGTTGATGTGATGATGAACGACGCTTTCACCGCAATGAGTGTGGAGGCG 308
 QY 82 MetProThrPheValPheLeuLysGluGlyLysGluValGluLysArgLeuValGlyAlaArg 102
 Db 309 AATGCCACATTTTGTCTTCAATTAAGATGGAAGAAAGATGACAGAGTGTGGTGCACAA 368
 QY 102 LysGluGluLeuGluAlaThrValGluLysHisGlyAla-----IleThrAla 118
 Db 369 GAAAGAGAGTGTGACAGACACCAATGAGAACGCTGCTCTCTACTGCTACTGCT 426
 RESULT 3

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 18:47:50 ; Search time 1825.46 Seconds

(without alignments)
2644.453 Million cell updates/sec

Title: US-09-786-715-4

Perfect score: 607

Sequence: 1 MASSEGGVICHSHVDENK.....YGAREKELQATVEKGAITA 118

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n model -DEV=xlp
-Q=/sgn2.1/USPRO/spool/US09786715/runat_11082003_150514_6035/app-query.fasta_1.1052
-DB=GenEmbl -QFMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blsum62 -TRANS=human4.0.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09786715.ecgn.1.1.5721.0runat_11082003_150514_6035 -NCPU=6 -ICPU=3
-NO_MMAP -LRGQUERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: GenEmbl:*
2: gb_ba:*
3: gb_hcg:*
4: gb_in:*
5: gb_com:*
6: gb_ov:*
7: gb_pat:*
8: gb_ph:*
9: gb_pl:*
10: gb_pr:*
11: gb_ro:*
12: gb_sts:*
13: gb_sy:*
14: gb_un:*
15: gb_vt:*
16: em_da:*
17: em_fun:*
18: em_hum:*
19: em_in:*
20: em_mu:*
21: em_om:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_un:*

29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hcg_hum:*
40: em_hcg_mus:*
41: em_hcg_other:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485.5	80.0	698	8	NTRNA
2	473.5	78.0	653	6	AR016869
3	473.5	78.0	653	6	AR020895
4	473.5	78.0	653	6	AR027218
5	473.5	78.0	653	6	AR038505
6	473.5	78.0	653	6	AR064647
7	473.5	78.0	653	6	AR067572
8	473.5	78.0	653	6	I38524
9	473.5	78.0	653	6	I56999
10	473.5	78.0	653	6	I59865
11	473.5	78.0	653	6	I75192
12	444	72.1	665	8	AY170650
13	442	72.8	603	8	RCYH10RXN
14	434	71.5	664	8	AF323593
15	432	70.2	593	8	PSA319808
16	425	70.0	595	8	D87984
17	422	69.5	630	8	PSA310990
18	419	69.0	345	6	AX505468
19	419	69.0	480	8	AY088687
20	419	69.0	497	8	ATPH10ARA
21	419	69.0	784	8	AY271308
22	406	66.9	345	8	AF483265
23	392	64.6	357	8	AY040028
24	392	64.6	528	8	ATTH1RED4
25	392	64.6	530	8	AK118035
26	392	64.6	560	8	AY087159
27	392	64.6	561	8	AF360227
28	390	64.3	526	11	G73679
29	390	64.3	601	8	OSU92541
30	390	64.3	686	6	E08194
31	390	64.3	687	8	RICTH
32	389	64.1	357	6	AX412276
33	389	64.1	357	6	AX412277
34	389	64.1	357	6	AX412278
35	389	64.1	357	6	AX412279
36	389	64.1	357	6	AX412279
37	389	64.1	357	6	AX412473
38	389	64.1	357	6	AX412474
39	389	64.1	357	6	AX412566
40	389	64.1	357	6	AX412917
41	389	64.1	357	6	AX507041
42	389	64.1	402	8	AX651357
43	389	64.1	440	8	AY114566
44	389	64.1	469	8	AY093318
45	389	64.1	489	8	AY065098
					ATTH1RED2

RESULT 1

ALIGNMENTS

recombinant cDNAs were transformed into E. coli XL1-Blue cells (Clontech). Suspensor cDNA plasmids used for directional sequencing were obtained by in vivo excision from the lambda Triplex2 recombinants in E. coli BM25.8 cells (Clontech).

BASE COUNT 154 a 92 c 134 g 190 t
ORIGIN

Alignment Scores:

Pred. No.:	8,31e-61	Length:	570
Score:	533.00	Matches:	100
Percent Similarity:	95.00%	Conservative:	14
Best Local Similarity:	83.33%	Mismatches:	6
Query Match:	86.67%	Indels:	0
DB:	14	Gaps:	0

US-09-786-715-6 (1-120) x CA901886 (1-570)

QY	1	MetaIaglySerSerGIUGlGlnValIleSerCysHisThrValGIUGlUTrPAsn	20
DB	82	ATGCCCGCGCATCAGAGGAGGAGCAAGTCATTCCTGCCACACCGTTGAGCATGGACA	141
QY	21	AspGlnLeuGlnIlySgIyAsnGluSerIlySleuIleValValAspPheThrAlaSer	40
DB	142	GAACAACCTCGAAAGGCGCAATTAATTCACAGAACTAATGTTGTGATTTACTGCTTCT	201
QY	41	TrpCysGlyProCysArgPheIleAlaProPheLeuAlaGIUleuAlaIlySlySPhetThr	60
DB	202	TGGTGTGACCATGCCGTTTCATTTCTCCATTTGGCTGAGCTGGCTAGAGAGTTTACA	261
QY	61	SerValIlePheLeuIlySValAspValAspGluLeuIlySerValSerGlnAspTrpAla	80
DB	262	AATGTCTATTCTGAGAGTGTGATGACGATTAAGAGTGTGCTGAAGATTTTGGCT	321
QY	81	IleGluAlaMetProThrPheValIleValIlySgIyThrLeuLeuAspIlyValVal	100
DB	322	GTTGAGGCAATGCCAAGCTTTGTGTGTGTGAAGAGGGAACCTTCTGGGCAAGTGTG	381
QY	101	GlyAlaIlySlyAspGluLeuGlnIlySleuIleGlnIlySHisValAlaSerAlaSerAla	120
DB	382	GGAGCAAGAAGAGAAATTCACAGACACATAGAGAAACATGTGGCTGCACCTAGTGTCT	441

Search completed: August 17, 2003, 23:34:21
Job time: 1628.86 secs

DB	Accession	Source	Organism	Definition	Location/Qualifiers
LOCUS	CD038084				
DEFINITION	UTPPI002.C04 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)				
ACCESSION	CD038084				
VERSION	CD038084.1				
KEYWORDS	EST				
SOURCE	Arachis hypogaea (peanut)				
ORGANISM	Arachis hypogaea				
REFERENCE	1 (bases 1 to 687)				
AUTHORS	Lu, M., Dang, P., Guo, B. Z., Holbrook, C. C., Lee, R. D., Bausner, M. G., and Lynch, R. E.				
TITLE	Generation and Analyses of ESTs for Arachis hypogaea				
JOURNAL	Unpublished				
COMMENT	Contact: Baozhu Guo USDA/ARS, Crop Protection and Management Research Unit 2747 Davis Rd., Tifton, GA 31794, USA Tel: 229-387-2334 Fax: 229-387-2321 Email: bguo@tifton.usda.gov Seq primer: T3.				
FEATURES					
SOURCE					
1..687					
/organism="Arachis hypogaea"					
/mol_type="mRNA"					
/cultivar="A13"					
/db_xref="taxon:3818"					
/clone="UTPPI002.C04"					
/tissue_type="Immature pods"					
/dev_stage="R6"					
/lab_host="XLI-Blue"					
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"					
/note="Vector: Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV1XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80°C freezer. Total RNA was isolated with TRIzol-Reagent ultrapur(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA GigaPack III Gold cloning Kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using GigaPack III Gold (Stratagene). The un-amplified library was used to excise pluscript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."					
BASE COUNT	189 a				
ORIGIN	107 c				
	176 g				
	215 t				
Alignment Scores:					
Pred. No.:	8.92e-64				
Score:	556.00				
Percent Similarity:	96.67%				
Best local Similarity:	85.83%				
Query Match:	90.41%				
DB:	14				
	Gaps:				
	0				

US-09-786-715-6 (1-120) x CD038084 (1-687)	US-09-786-715-6 (1-120) x CD038084 (1-687)
QY 1 MetalacylserSergluGlugluGlnvalIlesercysHsrhrValgluGluTrpAsn 20	QY 1 MetalacylserSergluGlugluGlnvalIlesercysHsrhrValgluGluTrpAsn 20
Db 69 ATGGCTGCTTCATCAGAAAGAGGACAGTATTCGCTGGTCCACCTCCGTTGATGATGCATGACC 128	Db 69 ATGGCTGCTTCATCAGAAAGAGGACAGTATTCGCTGGTCCACCTCCGTTGATGATGCATGACC 128
QY 21 AsplcInteugIntySGlYAsnGluSerLysLysLeuIleValValAspPheThrAlaSer 40	QY 21 AsplcInteugIntySGlYAsnGluSerLysLysLeuIleValValAspPheThrAlaSer 40
Db 129 CAAACAGCTCGAAGAGGAAATGAATCTAGAACGTCGATGTGTGTGATTCACAGCTTCA 188	Db 129 CAAACAGCTCGAAGAGGAAATGAATCTAGAACGTCGATGTGTGTGATTCACAGCTTCA 188
QY 41 TrpCysglYProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysIlyPheThr 60	QY 41 TrpCysglYProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysIlyPheThr 60
Db 189 TGTGTGGGACCATCCGCTTCATTCGACACCTTTCTGGCTGAGTTGGCTAAGAACTTTACA 248	Db 189 TGTGTGGGACCATCCGCTTCATTCGACACCTTTCTGGCTGAGTTGGCTAAGAACTTTACA 248
QY 61 SerValIlePheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAla 80	QY 61 SerValIlePheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAla 80
Db 249 AATGTCATATTTTGAAGGTGAGTCGATGCATCAACGTCGTTGCTTCAAGACTGGCCT 308	Db 249 AATGTCATATTTTGAAGGTGAGTCGATGCATCAACGTCGTTGCTTCAAGACTGGCCT 308
QY 81 IlleGluAlaMetProThrPheValPheValLysGluGluYThrIleLeuAspLysValVal 100	QY 81 IlleGluAlaMetProThrPheValPheValLysGluGluYThrIleLeuAspLysValVal 100
Db 309 GTGAGGCAATGCCACCCACCTTGTGTGTGTGAAAGAGGAAACCATTTATGACAAAGTGTG 368	Db 309 GTGAGGCAATGCCACCCACCTTGTGTGTGTGAAAGAGGAAACCATTTATGACAAAGTGTG 368
QY 101 GYValAlaLysAspGluLeuGlnGlnLysIlleGlnLysHisValAlaSerAlaSerAla 120	QY 101 GYValAlaLysAspGluLeuGlnGlnLysIlleGlnLysHisValAlaSerAlaSerAla 120
Db 369 GGACCAAGAAAGAAAGAACTGCACACAGAGCTTGAGAAACATGTGGCTACAGCCAGTGC 428	Db 369 GGACCAAGAAAGAAAGAACTGCACACAGAGCTTGAGAAACATGTGGCTACAGCCAGTGC 428
RESULT 15	RESULT 15
LOCUS CA901886 570 bp mRNA linear EST 27-DEC-2002	LOCUS CA901886 570 bp mRNA linear EST 27-DEC-2002
DEFINITION PCCS14170 Scarlet Runner Bean Suspensor Region Triplex2 Phaseolus	DEFINITION PCCS14170 Scarlet Runner Bean Suspensor Region Triplex2 Phaseolus
ACCESSION coccineus cDNA 5' similar to Thioedoxin H-type, mRNA sequence.	ACCESSION coccineus cDNA 5' similar to Thioedoxin H-type, mRNA sequence.
VERSION CA901886	VERSION CA901886
KEYWORDS CA901886.1 GI:27388878	KEYWORDS CA901886.1 GI:27388878
SOURCE EST.	SOURCE EST.
ORGANISM Phaseolus coccineus	ORGANISM Phaseolus coccineus
REFERENCE 1 (bases 1 to 570)	REFERENCE 1 (bases 1 to 570)
AUTHORS Bul,A.O., Le,B.H., Weerings,K., Bl,Y.-P., Choi,J.-S., McElroy,K.E.,	AUTHORS Bul,A.O., Le,B.H., Weerings,K., Bl,Y.-P., Choi,J.-S., McElroy,K.E.,
TITLE Choi,P.S., Harada,J.T., Fischer,R.L. and Goldberg,R.B.	TITLE Choi,P.S., Harada,J.T., Fischer,R.L. and Goldberg,R.B.
JOURNAL Gene Activity in Different Regions of a Post-Fertilization Plant	JOURNAL Embryo by EST Analysis
COMMENT Unpublished	COMMENT Unpublished
CONTACT: Goldberg, R.B.	CONTACT: Goldberg, R.B.
DEPARTMENT OF MOLECULAR, CELL, & DEVELOPMENTAL BIOLOGY	DEPARTMENT OF MOLECULAR, CELL, & DEVELOPMENTAL BIOLOGY
UNIVERSITY OF CALIFORNIA, LOS ANGELES	UNIVERSITY OF CALIFORNIA, LOS ANGELES
621 CHARLES E. YOUNG DRIVE SOUTH, LOS ANGELES, CA 90095-1606, USA	621 CHARLES E. YOUNG DRIVE SOUTH, LOS ANGELES, CA 90095-1606, USA
TEL: 310 825 3270	TEL: 310 825 3270
FAX: 310 825 8201	FAX: 310 825 8201
EMAIL: bobg@ucla.edu	EMAIL: bobg@ucla.edu
SEG PRIMER: 5' Triplex	SEG PRIMER: 5' Triplex
POLYA-NO.	POLYA-NO.
FEATURES	FEATURES
Source	Source
1..570	1..570
/organism="Phaseolus coccineus"	/organism="Phaseolus coccineus"
/mol_type="mRNA"	/mol_type="mRNA"
/culivar="Hammond's Dwarf Scarlet"	/culivar="Hammond's Dwarf Scarlet"
/db_xref="taxon:3886"	/db_xref="taxon:3886"
/dev_stage="6-days post-pollination"	/dev_stage="6-days post-pollination"
/clone_id="Scarlet Runner Bean Suspensor Region Triplex2"	/clone_id="Scarlet Runner Bean Suspensor Region Triplex2"
/note="Organ: Suspensor Region of Globular-Stage Embryos;	/note="Organ: Suspensor Region of Globular-Stage Embryos;
Vector: Triplex2; Site.1: SfiI; Site.2: SfiI; Suspensor	Vector: Triplex2; Site.1: SfiI; Site.2: SfiI; Suspensor
regions were micro-dissected from globular-stage embryos	regions were micro-dissected from globular-stage embryos
six days after pollination from greenhouse-grown plants	six days after pollination from greenhouse-grown plants
[Weerings et al., Plant Cell 13, 2409-2425 (2001)]	[Weerings et al., Plant Cell 13, 2409-2425 (2001)]
Double-stranded cDNA was synthesized from suspensor mRNA	Double-stranded cDNA was synthesized from suspensor mRNA
using the SMART cDNA Library Construction kit according to	using the SMART cDNA Library Construction kit according to
the manufacturer (Clontech). The suspensor cDNA fragments	the manufacturer (Clontech). The suspensor cDNA fragments
were directionally ligated into the SfiI restriction site	were directionally ligated into the SfiI restriction site
of the lambda Triplex2 vector (Clontech), and the	of the lambda Triplex2 vector (Clontech), and the


```

DB      355 GGAGCAAAAGAGTACGTCGACGACAGCAATAGCAATATGTCGCTCAGCTAGTGCCT 414
        ||||||||||||||||||||||||||| |||||||||||||||||||||||||||
RESULT 11
LOCUS   AM569018
DEFINITION
        AM569018 466 bp mRNA linear EST 03-DEC-2001
        s174e02.y1 Gm-cl031 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
        Gm-cl031-435 5' similar to TR:Q43636 Q43636 THIOREDOXIN. ;, mRNA
        sequence.
ACCESSION
        AM569018
VERSION
        AM569018.1 GI:7233673
KEYWORDS
        Glycine max (soybean)
SOURCE
        Glycine max
ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
        ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
        Glycine.
REFERENCE
        1 (bases 1 to 466)
AUTHORS
        Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corryell,V., Khanna
        ,A., Bolla,B., Matra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
        Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
        ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
        ,R., Ralster,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
        ,R., Materston,R. and Wilson,R.
TITLE
        Public Soybean EST Project
JOURNAL
        Unpublished
COMMENT
        Contact: Shoemaker R/Public Soybean EST Project
        Public Soybean EST Project
        Washington University School of Medicine
        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
        Tel: 314 286 1800
        Fax: 314 286 1810
        Email: est@watson.wustl.edu
        This clone is available through: Resgen, Invitrogen Corp. 2130
        South Memorial Parkway Huntville, AL 35801 For further information
        call: (800)-533-4363 or contact via email: cou@resgen.com
        High quality sequence stop: 416.
FEATURES
        source
        1..466
        Location/Qualifiers
            1..466
            /organism="Glycine max"
            /mol_type="mRNA"
            /db_xref="taxon:3847"
            /clone="GENOME SYSTEMS CLONE ID: Gm-cl031-435"
            /tissue_type="Williams seedlings, minus the cotyledons"
            /lab_host="DH10B"
            /clone_id="Gm-cl031"
            /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
            XhoI; This cDNA library was constructed from mRNA isolated
            from whole 'Williams' seedlings, minus the cotyledons,
            which were propagated on paper towels with distilled water
            for 5 days, incubated at 40 degrees C for 1 hour. The
            cotyledons were removed and the remaining tissue was
            flash-frozen in liquid nitrogen. Stratiagene's cDNA
            synthesis kit (catalog number 200401) was used to
            synthesize the cDNA. First-strand synthesis was performed
            with 5-methyl dcmp, hence the ligated cDNA was
            hemimethylated. A modification of Stratiagene's
            first-strand synthesis primer was used. An anchor'
            nucleotide (V-A, C, or G) was added to the 3' end of the
            primer [GAGAGAGAGAGAGAGAGAGACTGTGCGAG(T)18V] to anchor
            the primer at the 5' end of the poly(A) tract. After
            second strand synthesis, the cDNA ends were filled in with
            cloned pfu DNA, ligated to EcoRI adapters and
            subsequently phosphorylated. The cDNA was then
            precipitated and redissolved in sterile, RNase-,
            DNase-free water. The XhoI site within the first-strand
            synthesis primer was then restricted by digestion with
            XhoI from Promega (400/ul); all XhoI sites in the cDNA
            would be protected by their hemimethylated status. The
            cDNA constructs were size-fractionated with a 500 bp
            cutoff, using GibcoBRL Life Technologies' cDNA size
            Fractionation column. The column eluent was then

```

```

        precipitated, redissolved, and ligated into Stratiagene's
        pBluescript II XR predigested vector (pBluescript II SK(+))
        vector that has been digested with EcoRI and XhoI, and
        phosphorylated by Stratiagene). 100% of the white and blue
        colonies appear to contain recombinant plasmids with cDNA
        inserts, based on size (7-18 and 5, respectively). This
        library was constructed by Dr. Paul Keim and Dr. Virginia
        Corryell.
BASE COUNT      142 a      82 c      116 g      126 t
ORIGIN
Alignment Scores:
Pred. No.:      2,39e-67      Length:      466
Score:          581.00      Matches:      112
Percent Similarity: 97.508      Conservative: 5
Best Local Similarity: 93.33%      Mismatches: 3
Query Match:     94.47%      Indels:      0
DB:              Gaps:      0
US-09-786-715-6 (1-120) x AM569018 (1-466)
QY      1 MetAlaGlySerSerGluGluGluGluValIleSerCysHisThrValGluUtrPasn 20
        |||||||||||
DB      69 ATGGCAGGCTCCTCGGAGGAGGAGACAAATGATTAGCTGCACACCGTTGACCATGGCAAC 128
        |||||||||||
QY      21 AspgInLeuGlnIlyslGlnGlnIlyserIlyslIlyleValIlyAspPheThrAlaser 40
        |||||||||||
DB      129 GATCAACTCCAAAGAGGCAACCAATCCAAAGAACTCATTTGTGGATTTCCTGCTTCT 188
        |||||||||||
QY      41 TrpCysGlyProCysArpPheIleAlaProPheLeuAlaGluLeuAlaIlyslsPheThr 60
        |||||||||||
DB      189 TGGTGTGACCATGCCGTTTCATTCGACCATTTCTTGCGTACCTGGCTAAGAGTTCAACA 248
        |||||||||||
QY      61 SerValIlePheIleuIlyslValIlyslValIlyslValIlyslSerValSerGlnAspTrpAla 80
        |||||||||||
DB      249 AGTGTGCGATTCTCTTAAGAGTGATGGAGCAATTAAGAGTGTTCACAGACTGGCGCT 308
        |||||||||||
QY      81 IleGluAlaMetProThrPheValIlyPheValIlyGluGluIlyThrLeuIlyslsValIlyAl 100
        |||||||||||
DB      309 ATTGAGGCTATGCCCATTTTGTGTGGTGAAGAGGCAACCTTTAGCAAAAGTGGG 368
        |||||||||||
QY      101 GYAAlaIlyslsAspIlyleuGlnIlyslIleGlnIlyslsHisValAlaSerAlaSerAla 120
        |||||||||||
DB      369 GGAGCAAAAGAGATGAGCTGCACGACCAACAATAGAGAATATGTCGCTCAGCTAGTGCCT 428
        |||||||||||
RESULT 12
LOCUS   BG838879/c
DEFINITION
        BG838879 613 bp mRNA linear EST 25-MAY-2001
        GC01_06f08_R GC02_AAFc_ECORc_cold_stressed Glycine_clandestina_SSH
        Glycine clandestina cDNA clone GC01_06f08, mRNA sequence.
ACCESSION
        BG838879
VERSION
        BG838879.1 GI:14205201
KEYWORDS
        EST.
SOURCE
        Glycine clandestina
ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
        ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
        Glycine.
REFERENCE
        1 (bases 1 to 613)
AUTHORS
        Singh,J.A., Savole,A.J., Chapados,J., Courroux,P., De Moors,A.,
        Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and
        Tinker,N.A.
TITLE
        Differentially Expressed Sequence Tags from Cold-Stressed Glycine
        clandestina Seedlings
JOURNAL
        Unpublished
COMMENT
        Contact: Singh,J.A.
        Eastern Cereal and Oilseed Research Centre
        K.W. Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
        0C6, Canada
        Tel.: (613) 759-1662
        Fax: (613) 759-1701

```


material was provided by Michael G. Hahn (Complex Carbohydrate Research Center, University of Georgia) and the library was constructed by Anu Khanna (Lila Vodkin lab, University of Illinois).

BASE COUNT 142 a 97 c 120 g 163 t
ORIGIN

Alignment Scores:

Pred. No.: 2,05e-67 Length: 522
Score: 582.00 Matches: 113
Percent Similarity: 100.008 Conservative: 0
Best Local Similarity: 100.008 Mismatches: 0
Query Match: 94.63% Indels: 0
DB: 13 Gaps: 0

US-09-786-715-6 (1-120) x BQ786610 (1-522)

QY 8 GGLGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeuGlnValAsn 27
Db 1 GGACAGTCATTAGCTGCCACACCGTTGAAGATGCAACGATCACCAGAGGCGCAC 60
QY 28 GUSerLysLysLeuIleValAlaSpheThrAlaSerTrpCysGlyProCysArgPhe 47
Db 61 GAATCCAGAACTCATTTGTTGATTTACTGCTTCTGCTGAGCCATGCCGTTTC 120
QY 48 IleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIlePheLeuVal 67
Db 121 ATTGCACCATTTGGCTGGCTGAGCGCTAAGACAGTTCACAGTGCATATTCCTAAAGTG 180
QY 68 AspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAlaMetProThrPhe 87
Db 181 GAGTGGACGAATTAAGAGCTGTTTCACAGATTGGCTCATGAGGCTATGCCACTTTT 240
QY 88 ValPheValLysGluGluGluThrLeuAspLysValAlaGluValAlaLysAspGluLeu 107
Db 241 GTGTTTGTGAAGAGGACGCTTCTGCAAAAGTGGTGGAGCAAGAGATGACTG 300
QY 108 GlnGlnLysIleGlnLysHisValAlaSerAlaSerAla 120
Db 301 CACGAGAAATACAGAAACATGTCGCTTACGTAAGTCT 339

RESULT 10

LOCUS

AI988470 452 bp mRNA linear EST 30-NOV-2001

DEFINITION sc02107.y1 Gm-c1020 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1020-542 5' similar to TR:Q43636 Q43636 THIOREDOXIN.; mRNA

ACCESSION AI988470 GI:5820264

VERSION AI988470.1

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 452)

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corvett, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

TITLE

JOURNAL

COMMENT

Unpublished

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: Resgen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: cou@resgen.com

Seq primer: -40RP from Glibco

High quality sequence stop: 413.

Location/Qualifiers

1.452

/organism="Glycine max"

/mol_type="mRNA"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1020-542"

/tissue_type="root nodules of greenhouse grown plants"

/lab_host="XL10-Gold"

/clone_lib="Gm-c1020"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from nodules on the roots of 2.5 month-old Glycine max 'Williams' plants that were greenhouse grown. The cDNA library was prepared using the Stratagene pBluescript II SK(+) library construction kit. First strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A, C, or G) was added to the 3' end of the primer [GAGACAGAGAGAGAGAGACTGCTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase and size-fractionated with a 400 bp cutoff, using a SizeSeph 400 Spin column from Pharmacia. The column eluent was ligated to EcoRI adaptors and phosphorylated. The XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' cDNA size predicted vector (pBluescript II SK+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=56) and sequence (n=16). This library was constructed by Dr. Paul Keim and Dr. Virginia Corvett."

BASE COUNT

ORIGIN

136 a 80 c 113 g 123 t
Alignment Scores:
Pred. No.: 2.3e-67 Length: 452
Score: 581.00 Matches: 112
Percent Similarity: 97.50% Conservative: 5
Best Local Similarity: 93.33% Mismatches: 3
Query Match: 94.47% Indels: 0
DB: 9 Gaps: 0

US-09-786-715-6 (1-120) x AI988470 (1-452)

QY 1 MetAlaGlySerSerGluGluGlnValIleSerCysHisThrValGluGluTrpAsn 20
Db 55 ATGGCAGGCTCCCGAGGAGGAGCAAGCATTAAGCTGACACCGTTGACGATGGAGC 114
QY 21 AspGlnLeuGlnLysGlnSerLysLysLeuIleValAlaSpheThrAlaSer 40
Db 115 GATCAACTCCAGAGGACCAACATCCAGAACTATTTGTTGGATTTTACTGCTTCT 174
QY 41 TrpCysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThr 60
Db 175 TGGTGGAGACCAAGCGGTTTCATTTGACCATTTTGGCTGAGCTGCTAAGAGTTACA 234
QY 61 SerValIlePheLeuLysValAlaSerValLeuLysSerValSerGlnAspTrpAla 80
Db 235 AGTGTGATATCTTAAGGTCATGGATGGAGATTAAGAGTCTTCTCAAGACTGGCCT 294
QY 81 IleGluAlaMetProThrPheValIlePheValLysGluGluThrLeuLeuAspLysVal 100
Db 295 ATTGAGGCTATGGCCACTTTTGTGTTGAAGAGGAGCAACTTCTTAAGCAAGTGCG 354
QY 101 GtAlaLysLysAspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSerAla 120

ORGANISM	REFERENCE	TITLE	COMMENT	FEATURES
Glycine max	Enkaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: rosids ; eustoids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.			
	1 (bases 1 to 472)			
	Shoemaker, R., Kaim, P., Vodkin, L., Erpelting, J., Corvelli, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, J., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.			
	Public Soybean EST Project			
	Unpublished			
	Contact: Shoemaker R/Public Soybean EST Project			
	Public Soybean EST Project			
	Washington University School of Medicine			
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA			
	Tel: 314 286 1800			
	Fax: 314 286 1810			
	Email: est@wustl.edu			
	Putative full length read			
	vector to vector length is 622 This clone is available through:			
	Reagen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: cc@reagen.com			
	High quality sequence stop: 441.			
	Location/Qualifiers			
	1..472			
	/organism="Glycine max"			
	/mol_type="mRNA"			
	/db_xref="taxon:3847"			
	/clone="GENOME SYSTEMS CLONE ID: Gm-cl051-1569"			
	/tissue_type="floral meristematic mRNA"			
	/lab_host="DH10B"			
	/lab_id="Gm-cl051"			
	/note="Vector: plasmidscript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from floral meristematic mRNA provided by Dr. Halina Knap of Clemson University. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(AT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the plasmidscript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."			
	BASE COUNT	132 a	88 c	116 g
	ORIGIN			134 t
				2 others
	Alignment Scores:			
	Pred. No.:	1 33e-67	Length:	472
	Score:	583.00	Matches:	118
	Percent Similarity:	99.16%	Conservative:	0
	Best Local Similarity:	99.16%	Mismatches:	1
	Query Match:	94.80%	Indels:	1
		10	Gaps:	0
US-09-786-715-6 (1-120) x BE803058 (1-472)				
OY	2	AlaGlySerSerGluGluGlnValIleSerCysHisThrValGluGluTrpAsnAsp	21	
Db	15	GCTGCTCATCGAAGAGGCGACAGTCATTAGTGCACACCGTTGAAGATGGAACGAT	74	
OY	22	GlnLeuGlnLysGlyAsnGluSerLysLysLeuIleValValAspPheThrAlaSerTrp	41	
Db	75	CAACTCCAGAAAGGCAACGATCCAAAGAACTCATTTGTGGATTTTACGCTCTTGG	134	
OY	42	CysGlyProCysAspGlyPheIleAlaProPheLeuAlaGluLeuAlaLysPheThrSer	61	
Db	135	TGTGGACCATCGCGCTTTCATTCGACCACTTCTTGCGTCACTGCGTGAAGACTTACACAGT	194	

[illegible]

ORIGIN

Alignment Scores:

Pred. No.: 2,18e-71 Length: 445
 Score: 611.00 Matches: 119
 Percent Similarity: 99.17% Conservative: 0
 Best Local Similarity: 99.17% Mismatches: 1
 Query Match: 99.35% Indels: 0
 DB: 13 Gaps: 0

US-09-786-715-6 (1-120) x BU578741 (1-445)

QY 1 MetAlaGlySerSerGluGluGluValIleSerCysHisThrValGluGluTrpAsn 20
 Db 79 ATGCGTGGATGATCGGAAGAGGACAAAGTCAATTAGCGCCACACCGTTGAAGATGCAAC 138
 QY 21 AspGlnLeuGlnLysGlyAsnGlnSerLysLysLeuIleValAlaAspPheThrAlaSer 40
 Db 139 GATCACTCCAGAGGGGCAACGAATCCAGAAACTCATTTGTTGGATTCTTACTGCTTCT 198
 QY 41 TrpCysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThr 60
 Db 199 TGGTGTGACCATTCCTGTTCTTGGACACATTTCTGGCTGAGCTGGCTAAGAGTTGACA 258
 QY 61 SerValIlePheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAla 80
 Db 259 AGTGTCAATTCCTAAAGTGTGATGTGACGAATTAAGAGTGTTCATCAAGATTGGGCT 318
 QY 81 IleGluAlaMetProThrPheValIleValLysGluGluLysPheLeuAlaAspLysVal 100
 Db 319 ATTAGGCTATGCCACCTTTGTGTGTGAAGAGGGAACGCTTGGACAAAGTGTG 378
 QY 101 GlnAlaLysLysAspGluLeuGlnLysIleGlnLysHisValAlaSerAlaSerAla 120
 Db 379 GACACAAAGAGAGATGAGCTGCACAGCAAAATACAGAAACATGTGGCTTACGTAGTCT 438

RESULT 7

CA937588/c 572 bp mRNA linear EST 30-DEC-2002
 LOCUS sav21903.y1 Gm-c1048 glycine max cDNA clone SOYBEAN CLOVE ID:
 DEFINITION Gm-c1048-6078 5' similar to TR:Q43636 Q43636 THIOREDOXIN. ; mRNA
 sequence.

ACCESSION CA937588
 VERSION CA937588.1 GI:27426068
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: rosids
 ; eurosids I: Fabales: Fabaceae: Papilionoideae: Phaseoleae;
 Glycine.

1 (bases 1 to 572)
 Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corvelli,V., Khanna
 A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
 Wylie,T., Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers
 'T., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
 'R., Ritter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann
 'R., Waterston,R. and Wilson,R.

TITLE Unpublished
 JOURNAL Contact: Shoemaker R/Public Soybean EST project
 COMMENT Public Soybean EST project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu

This clone is available through: Resgen, Invitrogen Corp. 2130
 South Memorial Parkway Huntville, AL 35801 For further information
 call: (800)-533-4363 or contact: ccu@resgen.com web site:
 www.resgen.com
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40RP from Gibco

FEATURES

SOURCE

High quality sequence stop: 435.
 Location/Qualifiers

1..572
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLOVE ID: Gm-c1048-6078"
 /tissue_type="whole seedlings of greenhouse grown plants"
 /dev_stage="1 week old"
 /lab_host="DH10B"
 /clone_id="Gm-c1048"
 /note="Vector: pBluescript II SK+; site_1: EcoRI; site_2:
 XhoI; The Clark NTL was constructed and seed was provided
 by Dr. J. Specht, University of Nebraska (Shoemaker and
 Specht, 1995). The cDNA library was constructed from mRNA
 isolated from whole seedlings of 1 week old greenhouse
 grown plants. Complementary DNA was synthesized from mRNA
 using a primer consisting of a poly(dT) sequence with a
 XhoI restriction site and a 3' anchor. EcoRI adapters were
 ligated to the blunt-ended cDNA fragments followed by XhoI
 digestion. The cDNA fragments were directionally cloned
 into the EcoRI-XhoI restriction site of the pBluescript
 vector. The ligated cDNA fragments were transformed into
 DH10B host cells (GibcoBRL). The library was constructed
 in cooperation with Dr. Paul Keim's laboratory at Northern
 Arizona University."

BASE COUNT 174 a 125 c 102 g 171 t
 ORIGIN

Alignment Scores:

Pred. No.: 9.03e-70 Length: 572
 Score: 600.00 Matches: 117
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 97.56% Indels: 0
 DB: 14 Gaps: 0

US-09-786-715-6 (1-120) x CA937588 (1-572)

QY 4 SerSerGluGluGluGluValIleSerCysHisThrValGluGluTrpAsnAspGlnLeu 23
 Db 572 TCATCGGAAGAGGACCAAGTCAATTAGCTGCCACCCCTTAAGAAATGCAATCACTC 513
 QY 24 GlnLysGlyAsnGlnSerLysLysLeuIleValAlaAspPheThrAlaSerTrpCysGly 43
 Db 512 CAGAGGGCAACGAATCCAGAAACATGTTGTGATTTTCTGCTTCTTGTGTGGA 453
 QY 44 ProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIle 63
 Db 452 CCATGCCCTTTCATTCGACCATCTTGGCTGAGCTGCTAAGAAAGTTCACAAAGTGCATA 393
 QY 64 PheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAla 83
 Db 392 TTCCTTAAGGTGATGTGCGACGATTAAGAGTGTTCGAAAGTTGGCTATTGAGGCT 333
 QY 84 MetProThrPheValPheValLysGluGlyThrLeuLeuAspLysValAlaGlyAlaLys 103
 Db 332 ATGCCCACTTTTGTGTTGTGAAGAGGGAACGCTTGTGACAAAGTGTGGCGGCAAG 273
 QY 104 LysAspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSerAla 120
 Db 272 AAGATGAGCTGCAGCAGAAATACAGAAACATGTGCTTACCTAGTGTCT 222

RESULT 8

BE803058 472 bp mRNA linear EST 06-DEC-2001
 LOCUS BE803058
 DEFINITION st51c05.y1 Gm-c1051 glycine max cDNA clone GENOME SYSTEMS CLOVE ID:
 Gm-c1051-1569 5' similar to TR:Q43636 Q43636 THIOREDOXIN. ; mRNA
 sequence.

ACCESSION BE803058
 VERSION BE803058.1 GI:10224170
 KEYWORDS EST.
 SOURCE Glycine max (soybean)

Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-09-786-715-6 (1-120) x BG508580 (1-504)

OY 1 MetalaGlySerSerGluGluGlyGlnValIleSerCysHisThrValGluGluTrpAsn 20
 DB 37 ATGGCTGGCTCATCGAAGAGGAGGACAGCACTTACCTCCACACCGCTTGAGAAATGGAAC 96
 OY 21 AspGlnLeuGlnIlySgIyAsnGluSerIlySylLeuIleValValAspPheThrAlaSer 40
 DB 97 GATCAACTCCAGAAAGGACGCAATCCAAAGAACTCATGTTGTGGATTTCATCTCTCT 156
 OY 41 TrpCysGlyProCysArgPheIleAlaPheProPheLeuAlaGluLeuAlaIlySylSylPheThr 60
 DB 157 TGGTGTGGACCATGCCGTTTCATTTGCTACCATTTCTTGCTGAGCTGCTTAAGAGATTCA 216
 OY 61 SerValIlePheLeuIlySylValAspValAspGluLeuIlySerValSerGlnAspTrpAla 80
 DB 217 AGTGCATATTCCTTAAGCTGGATGGATGGACGAAATTAAGAGTGTTCACAGATTGGGCT 276
 OY 81 IleGluAlaMetProThrPheValAlaPheValIlySgIyGlyThrLeuLeuAspIlySylVal 100
 DB 277 ATTGAGCTATGCCACCTTTGTGTGTGTGAAGAGGAGCAACGCTTCTGACAACTGGTG 336
 OY 101 GlyAlaIlySylAspGluLeuGlnIlySylIleGlnIlySylHisValAlaSerAlaSerAla 120
 DB 337 GGAGCAAGAAAGATGAGCTGCAGCAAAATACAGAAATGATGCTTCACTGCTGCT 396

RESULT 4 B0630469 572 bp mRNA linear EST 21-OCT-2002
 LOCUS B0630469
 DEFINITION sag06f11.y1 Gm-cl045 glycine max cdna clone SOYBEAN CLONE ID: Gm-cl045-4125 5' similar to TR:Q43636 Q43636 THIOREDOXIN.; mRNA sequence.
 ACCESSION B0630469.1 GI:21678108
 VERSION B0630469.1
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 572)
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished
 COMMENT Contact: Shoemaker R./Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: coudresgen.com web site: www.resgen.com
 Seq primer: ~40RP from Gibco
 High quality sequence stop: 433.
 Location/Qualifiers

FEATURES
 Source 1..572

/organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-cl045-4125"
 /tissue_type="Hypocotyl, 9-10 day old etiolated seedlings"

/lab_host="DH10B"
 /clone_lib="Gm-cl045"
 /note="Vector: pBluescriptII SK+; Site 1: EcoRI; Site 2: XhoI. This cDNA library was constructed from mRNA isolated from etiolated hypocotyl tissue of 9-10 day old seedlings of the cultivar Williams 82. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) primer with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

BASE COUNT 160 a 105 c 134 g 173 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 8,87e-72 Length: 572
 Score: 615.00 Matches: 120
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-786-715-6 (1-120) x B0630469 (1-572)

OY 1 MetalaGlySerSerGluGluGlyGlnValIleSerCysHisThrValGluGluTrpAsn 20
 DB 52 ATGGCTGGCTCATCGAAGAGGAGGACAGCACTTACCTCCACACCGCTTGAGAAATGGAAC 111
 OY 21 AspGlnLeuGlnIlySgIyAsnGluSerIlySylLeuIleValValAspPheThrAlaSer 40
 DB 112 GATCAACTCCAGAAAGGACGCAATCCAAAGAACTCATGTTGTGGATTTCATCTCTCT 171
 OY 41 TrpCysGlyProCysArgPheIleAlaPheProPheLeuAlaGluLeuAlaIlySylSylPheThr 60
 DB 172 TGGTGTGGACCATGCCGTTTCATTTGCTACCATTTCTTGCTGAGCTGCTTAAGAGATTCA 231
 OY 61 SerValIlePheLeuIlySylValAspValAspGluLeuIlySerValSerGlnAspTrpAla 80
 DB 232 AGTGCATATTCCTTAAGCTGGATGGACGCAAAATGAGTGTTCACAGATTGGGCT 291
 OY 81 IleGluAlaMetProThrPheValAlaPheValIlySgIyGlyThrLeuLeuAspIlySylVal 100
 DB 292 ATTGAGCTATGCCACCTTTGTGTGTGTGAAGAGGAGCAACGCTTCTGACAACTGGTG 351
 OY 101 GlyAlaIlySylAspGluLeuGlnIlySylIleGlnIlySylHisValAlaSerAlaSerAla 120
 DB 352 GGAGCAAGAAAGATGAGCTGCAGCAAAATACAGAAATGATGCTTCACTGCTGCT 411

RESULT 5 B0630383 582 bp mRNA linear EST 21-OCT-2002
 LOCUS B0630383
 DEFINITION sag06f10.y1 Gm-cl045 glycine max cdna clone SOYBEAN CLONE ID: Gm-cl045-4100 5' similar to TR:Q43636 Q43636 THIOREDOXIN.; mRNA sequence.
 ACCESSION B0630383.1 GI:21678032
 VERSION B0630383.1
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 582)
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished
 COMMENT Contact: Shoemaker R./Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: coudresgen.com web site: www.resgen.com
 Seq primer: ~40RP from Gibco
 High quality sequence stop: 433.
 Location/Qualifiers

/db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-c1072-3915"
 /tissue_type="seedlings induced for symptoms of SDS
 (Sudden Death Syndrome) disease"
 /dev_stage="2-3 weeks old"
 /lab_host="DH10B"
 /clone_id="Gm-c1073"
 /note="Vector: plasmid II SK+, Site 1: EcoRI, Site 2:
 XhoI; The cDNA library was constructed from mRNA isolated
 from 2-3 week old seedlings that were induced for symptoms
 of SDS (Sudden Death Syndrome) disease by the
 translocation of culture filtrate of *Fusarium solani* f.
 sp. glyclines (Plant Cell Report 18:375-380). Cultivar
 Williams 82 is susceptible to the disease SDS. Plant
 tissue (expanded leaves, folded leaves, and new shoots)
 were collected at 1, 6, 24, and 48 hrs. after inoculation
 and their mRNA pooled equally for cDNA construction. The
 library was prepared using the Stratagene Bluescript II
 SK(+) library construction kit. Complementary DNA was
 synthesized from mRNA using a primer consisting of a
 poly(dT) sequence with an XhoI restriction site. EcoRI
 adaptors were ligated to the blunt-ended cDNA fragments
 followed by XhoI digestion. The cDNA insert is protected
 from XhoI digestion via methylation during first strand
 synthesis. The cDNA fragments were directionally cloned
 into the EcoRI-XhoI restriction site of the plasmid
 vector. The ligated cDNA fragments were transformed into
 E. coli Electromax DH10B host cells. Plants were inoculated
 by Shuxian Li (Glen Hartman lab, University of Illinois).
 Library was constructed by Reena Philip and Steve Clough
 (Lila Vodkin lab, University of Illinois)."

BASE COUNT 138 a 88 c 120 g 149 t
 ORIGIN

Alignment Scores:

Pred. No.: 7.31e-72 Length: 495
 Score: 615.00 Matches: 120
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-786-715-6 (1-120) x B0627882 (1-495)

QY 1 MetAlaGlySerSerGluGluGlnValIleSerCysHisThrValGluGluTrpAsn 20
 |||||
 Db 35 ATGGCGGCTCATCGAGAGGAGGACAGTCATTAGTCCACACCGTTGAAGATGAAC 94
 |||||
 QY 21 AspGlnLeuGlnLysGlnGluSerLysLysLeuIleValValAspPheThrAlaSer 40
 |||||
 Db 95 GATCAACTCCAGAGGAGGACAGCAATCCAAAGAACTCATTTGTGTCATTACGCTTCT 154
 |||||
 QY 41 TrpCysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThr 60
 |||||
 Db 155 TGGTGTGGACCAATGCCGTTTCATTCACCACTTGTGCTAGCGCTAAGAGTTGACA 214
 |||||
 QY 61 SerValIlePheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTyrPala 80
 |||||
 Db 215 AGTGTATATTTCTTAAGATGATGAGATTAAGAGCTTTTCTCAAGATTGGGCT 274
 |||||
 QY 81 IleGluAlaMetProThrPheValPheValLysGlnGluThrLeuLeuAspLysValVal 100
 |||||
 Db 275 ATTAGAGGCTATGCCCACTTTTGTGTTGTGAAGAGGAGCGCTTCGACAAAGTGTG 334
 |||||
 QY 101 GlyAlaLysLysAspGlnLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSerAla 120
 |||||
 Db 335 GGAAGCAAGAGATGAGTGCAGCAGAAATACAGAAACATGTGGCTCAGCTAGTGTCT 394
 |||||

RESULT 3

LOCUS B508580 504 bp mRNA linear EST 28-NOV-2001
 DEFINITION sac34f08.y1 Gm-c1072 glycine max cDNA clone GENOME SYSTEMS CLONE
 ID: Gm-c1072-1048 5' similar to TR:Q43636 Q43636 THIORDOXIN. ;

ACCESSION B508580
 VERSION B508580.1 GI:13479237
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

REFERENCE 1 (bases 1 to 504)
 Shoemaker, R., Kaim, P., Vodkin, L., Expelling, J., Coryell, V., Khanna
 A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers
 Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
 R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
 R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished

TITLE
 JOURNAL
 COMMENT
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

FEATURES
 source
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: ccu@resgen.com
 High quality sequence stop: 439.
 Location/Qualifiers

1..504
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1072-1048"
 /tissue_type="seedlings induced for symptoms of SDS
 (Sudden Death Syndrome) disease"
 /dev_stage="2-3 weeks old"
 /lab_host="DH10B"
 /clone_id="Gm-c1072"
 /note="Vector: Bluescript II SK+, Site 1: EcoRI, Site 2:
 XhoI; The cDNA library was constructed from mRNA isolated
 from 2-3 week old seedlings that were induced for symptoms
 of SDS (Sudden Death Syndrome) disease by the
 translocation of culture filtrate of *Fusarium solani* f.
 sp. glyclines (Plant Cell Report 18:375-380). Cultivar PI
 567374 is partially resistant to the disease SDS. Plant
 tissue (expanded leaves, folded leaves, and new shoots)
 were collected at 1, 6, 24, and 48 hrs. after inoculation
 and their mRNA pooled equally for cDNA construction. The
 library was prepared using the Stratagene Bluescript II
 SK(+) library construction kit. Complementary DNA was
 synthesized from mRNA using a primer consisting of a
 poly(dT) sequence with an XhoI restriction site. EcoRI
 adaptors were ligated to the blunt-ended cDNA fragments
 followed by XhoI digestion. The cDNA insert is protected
 from XhoI digestion via methylation during first strand
 synthesis. The cDNA fragments were directionally cloned
 into the EcoRI-XhoI restriction site of the plasmid
 vector. The ligated cDNA fragments were transformed into
 E. coli Electromax DH10B host cells. Plants were inoculated
 by Shuxian Li (Glen Hartman lab, University of Illinois).
 Library was constructed by Steve Clough (Lila Vodkin lab,
 University of Illinois)."

BASE COUNT 143 a 88 c 123 g 150 t
 ORIGIN

Alignment Scores:

Pred. No.: 7.49e-72 Length: 504
 Score: 615.00 Matches: 120
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

REFERENCE
AUTHORS

; eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 459)
Shoemaker, R., Keim, P., Vockin, L., Erpelting, J., Corvett, V., Khanna
, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
, R., Waterston, R., and Wilson, R.
Public Soybean EST Project

TITLE
JOURNAL
COMMENT

Unpublished
Contact: Shoemaker R./Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Putative full length read
vector to vector length is 527 This clone is available through:
Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL
35801 For further information call: (800)-533-4363 or contact via
email: ccul@resgen.com
Seq primer: -40RP from GIBCO
High quality sequence stop: 424.
Location/Qualifiers

FEATURES
SOURCE

1..459
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl081-878"
/tissue_type="Roots of 7 day old 'Brady' seedlings"
/dev_stage="7 days old"
/lab_host="DH10B"
/clone_lib="Gm-cl081"
/note="Vector: pBluescript II SK(+). Site 1: EcoRI, Site 2:
XhoI. The mRNA was isolated from roots of 7 day old
'Brady' seedlings that were mock-infected 48 hours prior
to harvest. Dr. Gary Stacey generously donated the
tissue. The roots were flash-frozen in liquid nitrogen.
Stratagene's cDNA Synthesis Kit (catalog number 200401)
was used to synthesize the cDNA. First-strand synthesis
was performed with 5-methyl dCTP, hence the ligated cDNA
was hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An 'anchor'
nucleotide (V-A, C, or G) was added to the 3' end of the
primer [GAGACAGACAGACAGACAGACTGCTGAG(T)18V] to anchor
the primer at the 5' end of the poly(A) tract. After
second-strand synthesis, the cDNA ends were filled in with
cloned Pfu DNA, ligated to EcoRI adapters and subsequently
phosphorylated. The cDNA was then precipitated and
redissolved in sterile, RNase-, DNase-free water. The XhoI
site within the first-strand synthesis primer was then
restricted by digestion with XhoI from Promega (400/ul);
all XhoI sites in the cDNA would be protected by their
hemimethylated status. The cDNA constructs were
size-fractionated with a 500bp cutoff, using Sephacryl
S-500 High Resolution (Pharmacia Biotech) in a 2 mm
diameter column and a bed volume of approximately 1ml. The
column eluent was precipitated, redissolved, and ligated
into Stratagene's pBluescript II XR predigested vector
(pBluescript II SK(+)) vector that has been digested with
EcoRI and XhoI, and phosphorylated by stratagene). This
library was constructed in the laboratory of Dr. Paul Keim
and Dr. Virginia H. Corvett at Northern Arizona
University."

BASE COUNT
ORIGIN

132 a 81 c 114 g 132 t

Alignment Scores:

Pred. No.: 6.61e-72 Length: 459
Score: 615.00 Matches: 120
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-786-715-6 (1-120) x B1699372 (1-459)

QY 1 MetAlaGlySerSergIuGluGlyGlnValIleSerCysHisThrValGluGluTrpAsn 20
DB 33 ATGGCTGGCTCATCGGAAGAGGACAGCATATGATGCTGCCACCGCTGAAGATGGAAC 92
QY 21 AspGlnLeuGlnIuGlyAsnGlnSerIuGlyLeuValValAspThrHisSer 40
DB 93 GATCAACTCCGCAAGGCGCAAGCAATCCAAAGCAATCATGTTGGATTTCACGCTCT 152
QY 41 TrpCysGlyProCysAtsPheIleAlaProPheLeuAlaGluLeuAlaIuGlyPheThr 60
DB 153 TGGTGTGGACCATCGCTTTCATTTGACCATTTCTGGCTGAGCTGCTAAAGATTGACA 212
QY 61 SerValIlePheLeuIuGlyValAspValAspIuLeuIuGlySerValSergIuAspTrpAla 80
DB 213 AGTGTCATATTCCTAAAGGTGATGATGAGCAATTAAGAGTGTTCAGAGATTGGGCT 272
QY 81 IleGluAlaMetProThrPheValAlaPheValIuGlyThrLeuAspIuValVal 100
DB 273 ATTGAGGCTATGCCACACTTTGTGTGTGAAGAGGACGCTTCGGACAAAGTGCTG 332
QY 101 GlyValAluIuGlyAspGluLeuGlnGlnIleGlnIuGlyHisValAlaSerAla 120
DB 333 GGAGCAAGAGAGATGACTGCTGACACCAAAATACAGAACATGTGGCTTCAGCTAGTCT 392

RESULT 2
LOCUS B0627882 495 bp mRNA linear EST 02-JUL-2002
DEFINITION sa65502.y2 Gm-cl073 glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl073-3915 5' similar to TR:Q43636 Q43636 THIOREDOXIN.; mRNA

ACCESSION B0627882
VERSION B0627882
KEYWORDS B0627882.1 GI:21675531
SOURCE EST.
ORGANISM Glycine max (soybean)

Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
AUTHORS

1 (bases 1 to 495)
Shoemaker, R., Keim, P., Vockin, L., Erpelting, J., Corvett, V., Khanna
, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
, R., Waterston, R., and Wilson, R.
Public Soybean EST Project

TITLE
JOURNAL
COMMENT

Unpublished
Contact: Shoemaker R./Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccul@resgen.com web site:
www.resgen.com
Putative full length read
vector to vector length is 605
Seq primer: -40RP from GIBCO
High quality sequence stop: 420.
Location/Qualifiers

FEATURES
SOURCE

1..495
/organism="Glycine max"
/mol_type="mRNA"

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 19:20:27 ; Search time 1622.86 Seconds
(without alignments)
1797.162 Million cell updates/sec

Title: US-09-786-715-6
Perfect score: 615
Sequence: 1 MAGSSEGVVSCHTVEWNN.....GAKKDELOQIKKHVASASA 120

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n model -DBV=ylp
-Q/cgnt2.1/USFTO.spool/US09786715/runat_11082003_150514_6048/app_query.fasta.1.1052
-DB=EST -QFMT=fastap -SUFFIX=1st -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=psco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USFR=US09786715 @CGN_1.1.7834 @runat_11082003_150514_6048 -NCP=6 -ICPU=3
-NO_MMAP -LARGEIOBURN -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMECUT=120 -WARN_TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST: *
1: em_estba: *
2: em_esthum: *
3: em_estlin: *
4: em_estinu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_luv: *
19: em_gss_pln: *
20: em_gss_vlt: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_tod: *
26: em_gss_ping: *
27: em_gss_vrl: *
28: gb_gss1: *

29: gb_gss2: *
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	615	100.0	459	12	B1699372 sag36c07.
2	615	100.0	495	13	B0627882 sac05b02.
3	615	100.0	504	10	BG508580 sac74f08.
4	615	100.0	572	13	B0630459 sac07f11.
5	615	100.0	582	13	B0630383 sac06f10.
6	611	99.3	445	13	B0578741 sar60h12.
7	600	97.6	572	14	CA937588 sar21g03.
8	583	94.8	472	10	BE803058 sr51c05.y
9	582	94.6	522	13	B0786610 sac70f04.
10	581	94.5	452	9	A1988470 s02f07.y
11	581	94.5	466	9	AW569018 s174e02.y
12	577	93.8	613	12	BG838879 GC01_06f0
13	566	92.0	627	14	CD401101 GM_CK2312
14	556	90.4	687	14	CD038084 UHPPI002
15	533	86.7	570	14	CA901886 PCS14170
16	528	85.9	572	14	CA411141 E834_F-P
17	515	83.7	632	14	CA896875 PCEP05423
18	512	83.3	445	10	BE610138 sag62b12.y
19	512	83.3	512	14	CA794815 CAG_BL_18
20	502	81.6	498	14	CA901885 PCS11713
21	501	81.5	311	12	B1094898 sae01e08.
22	500	81.3	537	13	B0625213 USDA-FP_0
23	500	81.3	655	14	CB291687 UCRCS01_0
24	497	80.8	653	14	CB293759 UCRCS01_0
25	495	80.5	517	14	CA795737 CAG_BL_27
26	494	80.3	654	14	CB291686 UCRCS01_0
27	490	79.7	394	14	CA901887 PCS15426
28	490	79.7	493	14	CB303550 WSA0001.L
29	490	79.7	546	10	BE053835 GA_Ea000
30	485	78.9	480	13	B0822062 UB32BPB12
31	485	78.9	555	13	B0875659 V009G01.P
32	485	78.9	564	14	CA825633 R63G02.P
33	485	78.9	587	13	B0863412 S027G05.P
34	485	78.9	622	9	AW255457 M4A80.pcp
35	483	78.5	579	14	CA825259 R36B03.LW
36	481	78.2	448	14	CA824794 R48E08.LW
37	480	78.0	581	14	CA824034 R35D03.LW
38	475.5	77.3	543	14	CB077020 h147g06.y
39	470	76.4	634	9	AU300651 AU300651
40	469	76.3	586	9	AW255195 ML185.pcp
41	468	76.1	316	12	B1892660 saf36d06.
42	468	76.1	413	14	T24347 crs1466.lam
43	467	75.9	540	14	CB377001 HB02G03.L
44	467	75.9	602	10	BE054543 GA_Ea002
45	466	75.8	523	12	BM11010 EST58546

ALIGNMENTS

RESULT 1
B1699372
LOCUS
DEFINITION B1699372 459 bp mRNA linear EST 29-NOV-2001
sag36c07.y1 Gm-cl081 glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl081-878 5' similar to TR:Q43636 Q43636 THIOREDOXIN. ;
RNA sequence.
B1699372
ACCESSION B1699372.1 GI:15662001
VERSION
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

US-09-786-715-6 (1-120) x US-10-091-841-5 (1-393)

QY 8 GlnGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeuGlnIlysgIysn 27
DB 61 GGGGAGGTGATCTCCGTCACAGCCTGGAGCAGTGCACCATCGACAGAGGCCAAC 120
QY 28 GluSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCysArgPhe 47
DB 121 GCGCCAGAGAGCTGTGTGTGATTGACTTCACTGCATCATGTGTGGGACCAATGCCCAT 180
QY 48 IleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIlePheLeuLysVal 67
DB 181 ATGCTCCAAATTTTGGTGTGATCTCCGCAAGAGTTCCAGCTGCTTTTCTCAAGGTC 240
QY 68 AspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAlaMetProThrPhe 87
DB 241 GACGTTGATGAACTGAAGCCCATCTGAGCAATTCAGGCTGAGGCCATGCCAACCTTC 300
QY 88 ValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLysLysAspGluLeu 107
DB 301 CTGTTCAATGAGGAGAGAGAGCTCAAGACAGAGGTTGTGAGCTATCATAGAGAGGCTG 360
QY 108 GlnGlnLysIleGlnLysHisValAlaSer 117
DB 361 ACGACCAAGGTTGGCTCCACGCGGCTGCC 390

RESULT 13
US-10-091-841-3
; Sequence 3, Application US/10091841
; Publication No. US20030150010A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; FILE REFERENCE: 2001-0701.30
; CURRENT FILING DATE: 2002-03-05
; PRIOR FILING DATE: 09/540, 014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: wheat thioredoxin h cDNA
US-10-091-841-3

Alignment Scores:
Pred. No.: 5,38e-45 Length: 382
Score: 367.00 Matches: 63
Percent Similarity: 81.65% Conservative: 26
Best Local Similarity: 57.80% Mismatches: 20
Query Match: 59.67% Indels: 0
Gaps: 0

US-09-786-715-6 (1-120) x US-10-091-841-3 (1-382)

QY 8 GlnGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeuGlnIlysgIysn 27

DB 52 GGGGAGGTGATCTCCGTCACAGCCTGGAGCAGTGCACCATCGACATCGAGAGGCCAAC 111
QY 28 GluSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCysArgPhe 47
DB 112 GCGCCAGAGAGCTGTGTGTGATTGACTTCACTGCATCATGTGTGGGACCAATGCCCAT 171
QY 48 IleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIlePheLeuLysVal 67
DB 172 ATGCTCCAAATTTTGGTGTGATCTCCGCAAGAGTTCCAGCTGCTTTTCTCAAGGTC 231
QY 68 AspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAlaMetProThrPhe 87
DB 232 GACGTTGATGAACTGAAGCCCATCTGAGCAATTCAGGCTGAGGCCATGCCAACCTTC 291
QY 88 ValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLysLysAspGluLeu 107
DB 292 CTGTTCAATGAGGAGAGAGATGTCAAGACAGGTTGTGAGCTATCATAGAGAGAACATG 351
QY 108 GlnGlnLysIleGlnLysHisValAla 116
DB 352 ACGACCAAGGTTGGCTACACGCGGCC 378

RESULT 14
US-10-194-885-8
; Sequence 8, Application US/10194885
; Publication No. US20030135878A1
; GENERAL INFORMATION:
; APPLICANT: Wong, J. H.
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH ELEVATED
; FILE REFERENCE: 416272000800
; CURRENT FILING DATE: 2002-07-12
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US/10/194,885
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/538,864
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/126,736
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Barley
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(369)
US-10-194-885-8

Alignment Scores:
Pred. No.: 3,97e-44 Length: 369
Score: 361.00 Matches: 62
Percent Similarity: 81.65% Conservative: 27
Best Local Similarity: 56.88% Mismatches: 20
Query Match: 58.70% Indels: 0
Gaps: 0

US-09-786-715-6 (1-120) x US-10-194-885-8 (1-369)

QY 9 GlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeuGlnIlysgIysn 28
DB 37 GAGTGATCTGCTCCGTCACAGCCTGGAGCAGTGCACCATCGACATCGAGAGGCCAACACC 96
QY 29 SerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCysArgPhe 48
DB 97 GCCAAGAGAGCTGTGTGATTGACTTCACTGCATCATGTGTGGGACCAATGCCCATCATG 156
QY 49 AlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIlePheLeuLysValAsp 68

SDO ID NO 1736
 LENGTH: 357
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1736

Alignment Scores:

Pred. No.: 1.9e-46 Length: 357
 Score: 376.50 Matches: 67
 Percent Similarity: 80.87% Conservative: 26
 Best Local Similarity: 58.26% Mismatches: 19
 Query Match: 61.22% Indels: 3
 Gaps: 1

US-09-786-715-6 (1-120) x US-09-938-842A-1736 (1-357)

QY 7 GluGluGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeuGlnLysGly 26
 Db 10 GAAGGAGAGATTATCGCTTGGCCACACCGTTGAGATTGGACCGAGAGCTCAAGCCGCC 69
 QY 27 AsnGluSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCysArg 46
 Db 70 AACGAATCCAAAGAACTGATTGTGATGACTTCACTGCAACATGCTGCCACCTTGCCT 129
 QY 47 PheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIlePheLeuLys 66
 Db 130 TTCATTGCCACCGCTTCTTGGCTGACTTGCACAGAACACCTCGACGTAGCTTCTTCAG 189
 QY 67 ValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAlaMetProThr 86
 Db 190 GTGCATGTTGACGAATTGAAACACCTGTTGCTGAGAGATTAAAGTTCAAGGCAATCCACAG 249
 QY 87 PheValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLysAspGlu 106
 Db 250 TTATCTTCATGAAAGAGAGAGATCAAGAGACTGTGGTGTGCTGCTGAAGAGAA 309
 QY 107 LeuGlnGlnLysIleGlnLysHis-----ValAlaSerAla 118
 Db 310 ATCATTGCCAATCTCGAAGACACAGACAGTGTGTCTGTCTGCT 354

RESULT 11

US-10-323-362-1
 Sequence 1, Application US/10323362
 Publication No. US20030113786A1
 GENERAL INFORMATION:
 APPLICANT: Kurnik, Betsy
 APPLICANT: Davis, Keith
 APPLICANT: Zayed, Adel
 APPLICANT: Ascenzi, Robert
 APPLICANT: Harper, Angel
 APPLICANT: Boyes, Douglas
 APPLICANT: Mulpuri, Rao
 APPLICANT: Hoffman, Neil
 APPLICANT: Kjemtrup, Susanne
 APPLICANT: Moessner, Jeffrey
 APPLICANT: Gorlach, Jorn
 APPLICANT: Hamilton, Carol
 TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF INHIBITORS OF THIOREDOXIN EXPRESSION
 FILE REFERENCE: 2133US
 CURRENT APPLICATION NUMBER: US/10/323,362
 CURRENT FILING DATE: 2002-12-18
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 357
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 US-10-323-362-1

Alignment Scores:
 Pred. No.: 1.9e-46 Length: 357
 Score: 376.50 Matches: 67

Percent Similarity: 80.87% Conservative: 26
 Best Local Similarity: 58.26% Mismatches: 19
 Query Match: 61.22% Indels: 3
 Gaps: 1

US-09-786-715-6 (1-120) x US-10-323-362-1 (1-357)

QY 7 GluGluGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeuGlnLysGly 26
 Db 10 GAAGGAGAGATTATCGCTTGGCCACACCGTTGAGATTGGACCGAGAGCTCAAGCCGCC 69
 QY 27 AsnGluSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCysArg 46
 Db 70 AACGAATCCAAAGAACTGATTGTGATGACTTCACTGCAACATGCTGCCACCTTGCCT 129
 QY 47 PheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIlePheLeuLys 66
 Db 130 TTCATTGCCACCGCTTCTTGGCTGACTTGCACAGAACACCTCGACGTAGCTTCTTCAG 189
 QY 67 ValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAlaMetProThr 86
 Db 190 GTGCATGTTGACGAATTGAAACACCTGTTGCTGAGAGATTAAAGTTCAAGGCAATCCACAG 249
 QY 87 PheValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLysAspGlu 106
 Db 250 TTATCTTCATGAAAGAGAGATCAAGAGACTGTGGTGTGCTGCTGAAGAGAA 309
 QY 107 LeuGlnGlnLysIleGlnLysHis-----ValAlaSerAla 118
 Db 310 ATCATTGCCAATCTCGAAGACACAGACAGTGTGTCTGTCTGCT 354

RESULT 12

US-10-091-841-5
 Sequence 5, Application US/10091841
 Publication No. US20030150010A1
 GENERAL INFORMATION:
 APPLICANT: Cho, Myeong-Je
 APPLICANT: Del Val, Greg
 APPLICANT: Gallau, Maxime
 APPLICANT: Lemaux, Peggy G.
 APPLICANT: Buchanan, Bob B.
 TITLE OF INVENTION: Barley Gene for Thioredoxin and
 FILE REFERENCE: NADP-Thioredoxin Reductase
 CURRENT APPLICATION NUMBER: US/10/091,841
 CURRENT FILING DATE: 2002-03-05
 PRIOR APPLICATION NUMBER: 09/540,014
 PRIOR FILING DATE: 2000-03-31
 PRIOR APPLICATION NUMBER: US 60/127,198
 PRIOR FILING DATE: 1999-03-31
 PRIOR APPLICATION NUMBER: US 60/169,162
 PRIOR FILING DATE: 1999-12-06
 PRIOR APPLICATION NUMBER: US 60/177,740
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: US 60/177,739
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 51
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 5
 LENGTH: 393
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: wheat thioredoxin h cDNA
 US-10-091-841-5

Alignment Scores:
 Pred. No.: 3.99e-45 Length: 393
 Score: 368.00 Matches: 63
 Percent Similarity: 81.82% Conservative: 27
 Best Local Similarity: 57.27% Mismatches: 20
 Query Match: 59.84% Indels: 0
 Gaps: 0

Db 369 GACCTTCAGCCACCATA 386

RESULT 8
US-10-349-782-12
; Sequence 12, Application US/10349782
; Publication No. US20030143618A1
; GENERAL INFORMATION:
; APPLICANT: Yves Hatzfeld
; APPLICANT: Valerie Marie-No. US20030143618A1lle Frankard
; APPLICANT: Anne-Marie Droual
; TITLE OF INVENTION: Method for easy cloning and selection of chimeric DNA molecules
; FILE REFERENCE: 1187-15
; CURRENT APPLICATION NUMBER: US/10/349,782
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: EP 02075373.7
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; LENGTH: 540
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified thioredoxin of *Oryza sativa* in vector pDONR201
US-10-349-782-12

Alignment Scores:
Pred. No.: 9,71e-48 Length: 540
Score: 387.00 Matches: 72
Percent Similarity: 77.69% Conservative: 22
Best Local Similarity: 59.50% Mismatches: 23
Query Match: 62.93% Indels: 4
DB: 12 Gaps: 1

US-09-786-715-6 (1-120) x US-10-349-782-12 (1-540)

QY 4 SerSerGluGluGlyGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeu 23
Db 61 GCGCGCAGAGGAGGAGGAGTGTGATCGGCTCCACACACAGAGAGTTCACGCCGAGAG 120

QY 24 GlnLysGlyAsnGluSerLysLysLeuIleValAlaAspPheThrAlaSerTrpCysGly 43
Db 121 ACCAAGGCCAAGAGGCGCCGCAAGGTCATATGACTTCACCTCTCTCGTGGTCGGA 180

QY 44 ProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrValIle 63
Db 181 CCGTCCCGCTTCATCGCCCGGAGTGTTCGCTGAATACGCCCAAAAGTTCCTCGTGTGTC 240

QY 64 PheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAla 83
Db 241 TTCCCTGAAGGTTGATGTTTATGATGAGCTGAAGAGAGTTGCTGAAGAGTATGTCGAGGCA 300

QY 84 MetProThrPheValAlaPheValLysGluGlyThrLeuLeuAspLysValAlaGlyAlaLys 103
Db 301 ATGCCGACCTTCCTATTCATCAAGATGTCGTCGAGGCTGACAAAGTCTGGCGCCAGG 360

QY 104 LysAspGluLeuGlnGlnLysIleGlnLysHisVal-----AlaSerAlaSer 119
Db 361 AAGGATGACCTTCAGAACACACATCGTGAAGCACGTCGTCACCTGTCATCTGCTCT 420

QY 120 Ala 120
Db 421 GCC 423

RESULT 9
US-09-938-842A-164
; Sequence 164, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCDIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 164
; LENGTH: 360
; TYPE: DNA
; ORGANISM: *Arabidopsis thaliana*
US-09-938-842A-164

Alignment Scores:
Pred. No.: 3,48e-47 Length: 360
Score: 381.50 Matches: 72
Percent Similarity: 77.12% Conservative: 19
Best Local Similarity: 61.02% Mismatches: 26
Query Match: 62.03% Indels: 1
DB: 10 Gaps: 1

US-09-786-715-6 (1-120) x US-09-938-842A-164 (1-360)

QY 4 SerSerGluGluGlyGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeu 23
Db 4 GCGCGCAGAGGAGGAGGAGTGTGATCGGCTCCACACAGAGAGTTCACGCCGAGAG 63

QY 24 GlnLysGlyAsnGluSerLysLysLeuIleValAlaAspPheThrAlaSerTrpCysGly 43
Db 64 GATAAAGCCCAAAACCAACAGCGATGATGATTGATTGATTCACCTCTTCAGTGTGCA 123

QY 44 ProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPhe--ThrSerVal 62
Db 124 CCAATGCCGATGATGCTTCATTCATTCACAGATTTGGCCAGAGATTCATGCAATGCC 183

QY 63 IlePheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGlu 82
Db 184 ACTTCTTCAGAGGTGATGTCGATGAACTTCAGAGGTGTCCTTAAGATTTGGTGTGAG 243

QY 83 AlaMetProThrPheValAlaPheValLysGluGlyThrLeuLeuAspLysValAlaGlyAla 102
Db 244 GCATGCCCAACCTTGTGTTCAATTAAGCCGCGGAGGTTGTGATGAAGCTCGTGTGCG 303

QY 103 LysLysAspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSerAla 120
Db 304 AATAAAGAGATCTTCAGCGCAAAATATGAGACATACCTGCTGTACAACTGCC 357

RESULT 10
US-09-938-842A-1736
; Sequence 1736, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCDIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379

Alignment Scores:

Pred. No.: 1.71e-55 Length: 402
Score: 438.00 Matches: 81
Percent Similarity: 84.21% Conservative: 15
Best Local Similarity: 71.05% Mismatches: 18
Query Match: 71.22% Indels: 0
DB: 10 Gaps: 0

US-09-786-715-6 (1-120) x US-09-878-574-3723 (1-402)

QY 5 SerGluGluGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeuGln 24
DB 46 GCGGAAGAGGACAAAGATGCGTGTCCACGCGTAGAGGAGGAACATCTCAAG 105
QY 25 LysGlyAsnGluSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyPro 44
DB 106 AAGGAGAGAGGACCAAGAAATGATTGTGTGATTTTCTGCTTCTTGTGCGGTCGA 165
QY 45 CysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIlePhe 64
DB 166 TGGCGTTTCATTCGCCCAATTCCTTGACAGATTGCTPAAAAAGTTGCCGAAATGTCACCTTC 225
QY 65 LeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAlaMet 84
DB 226 CTCACGCTGATGTGATGATGATGAGACTGTTCCACAGCAGTGGGCAATTGAGGCTATG 285
QY 85 ProThrPheValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLysLys 104
DB 286 CCACCTTCCTCTGTTTGAAGAAGACGACGCTGTGACAGAGTTGGTGGTCCACACAA 345
QY 105 AspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAla 118
DB 346 GAGGAGCTGCATTTGACCTACGACAGACATGCGCAACTGCC 387

RESULT 6

US-09-878-574-104
; Sequence 104, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 104
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-056-Q1-B1-B3
US-09-878-574-104

Alignment Scores:

Pred. No.: 1.96e-53 Length: 392
Score: 424.00 Matches: 77
Percent Similarity: 86.21% Conservative: 23
Best Local Similarity: 66.38% Mismatches: 16
Query Match: 68.94% Indels: 0
DB: 10 Gaps: 0

US-09-786-715-6 (1-120) x US-09-878-574-104 (1-392)

QY 5 SerGluGluGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeuGln 24
DB 9 GCGAAGAGGCTCAGCTTGTGCGCTCCACACCGTGTGATGCAACGACGCAACTGCAG 68
QY 25 LysGlyAsnGluSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyPro 44

DB 69 AATGAAAGACTCCCAAAATGATTGTGTGATTTTACTGCTTCCTGTGTGTCCA 128

QY 45 CysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIlePhe 64
DB 129 TGGCGTTTATTGCCCCAGTTCGTGACAGATTGCTTAGGCAATCTCTCAAGTATCTTC 188

QY 65 LeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAlaMet 84
DB 189 CTCACGCTGATGTGATGAGTAGAGGCTGTGCTGAGGAATATTCATTGAGGCCATG 248

QY 85 ProThrPheValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLysLys 104
DB 249 CCACCTTCCTCTTCTTGAAGAAGTGCACAGATCTGTGATAGGTTGTTGTGCTTAAGCAG 308

QY 105 AspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAla 120
DB 309 GAGGAGCTGCACACTCACCATAGCCACATGATGATCTGCTGCTGT 356

RESULT 7

US-09-878-574-1462
; Sequence 1462, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1462
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-037-Q1-B1-F11
US-09-878-574-1462

Alignment Scores:
Pred. No.: 1.53e-48 Length: 390
Score: 391.00 Matches: 72
Percent Similarity: 84.91% Conservative: 18
Best Local Similarity: 67.92% Mismatches: 16
Query Match: 63.58% Indels: 0
DB: 10 Gaps: 0

US-09-786-715-6 (1-120) x US-09-878-574-1462 (1-390)

QY 6 GluGluGlnGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeuGlnLys 25
DB 69 GAAAGAGGACAGGTCATCGGCTCCACACCGTGTGATGAGTGACGTCACGATTCGAAT 128
QY 26 GlyAsnGluSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGlyProCys 45
DB 129 GCAAAAGACTCCAAAAACGATTTGTGTGATTTTACTGCTTCCTGCTGTGTCATGTC 188
QY 46 ArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIlePheLeu 65
DB 189 CGTTTATGCCCCCAGTTCGTGACAGATTGCAAAAGAACTCCTGAAATGATCTTCCTC 248
QY 66 LysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAlaMetPro 85
DB 249 AAGGTGATGTGATGATGAGGAGGCTGTGCTGAGGAAATATTCATTGAGGCCATGCCA 308
QY 86 ThrPheValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLysLysAsp 105
DB 309 ACCTTCCTCTTCTTGAAGAAGTGCAGATGCTGACAAAGTGTGTGCTACTAGATGAT 368
QY 106 GluLeuGlnGlnLysIle 111

```
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 3129
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1555)..(1896)
US-09-897-898-5

Alignment Scores:
Pred. No.: 1,06e-60 Length: 3129
Score: 482.00 Matches: 88
Percent Similarity: 89.38% Conservative: 13
Best Local Similarity: 77.88% Mismatches: 12
Query Match: 78.37% Indels: 0
DB: Gaps: 0

US-09-786-715-6 (1-120) x US-09-897-898-5 (1-3129)
QY 4 SerSerGluGluGlyGlnValIleSerCysHisThValGluGluTrpAsnAspGlnLeu 23
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1558 GCTTCGGAAGAGACAAAGTATCGCTCCACACCGTTGAGACATGGAACGACGAGCTT 1617
QY 24 GlnYsGlyAsnGluSerLysLysLeuIleValIleValAspPheThrAlaSerTrpCysGly 43
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1618 CAGAAAGCTAATGAATCCAAACTCTTGCTGGTGATTTACGGCTCTTGCTGGA 1677
QY 44 ProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIle 63
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1678 CCGATGCGTTTCATCGCTCCATCTTCTTGCTGATTTGGCTAGAACTTCTTAACGTCCTT 1737
QY 64 PheLeuLysValAspValAspLysLysLysLysLysLysLysLysLysLysLysLysLys 83
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1738 TTCCTCAAGGTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1797
QY 84 MetProThrPheValPheValLysGluGlyThrLeuLeuAspLysValIleGlyAlaLys 103
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1798 ATGCCAACCTTCATGTTTGAAGGAGGAGATTTGGACAAAGTTGTGGAGCCAG 1857
QY 104 LysAspGluLeuGlnGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1858 AAAGATGAGCTTCAGTCTACATTCGCAACACTTGCGCT 1896

RESULT 4
US-09-897-898-7
/ Sequence 7, Application US/09897898
/ Patent No. US20020037303A1
/ GENERAL INFORMATION:
/ APPLICANT: DECKERS, HARM M.
/ APPLICANT: VAN ROOIJEN, GJOS
/ APPLICANT: BOOTHIE, JOSEPH
/ APPLICANT: GOLT, JANIS
/ APPLICANT: MOLONEY, MAURICE M.
/ APPLICANT: DALMIA, BIPIN K.
/ TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
/ FILE REFERENCE: 034547/0104
/ CURRENT APPLICATION NUMBER: US/09/897,898
/ CURRENT FILING DATE: 2001-09-21
/ PRIOR APPLICATION NUMBER: 09/577,147
/ PRIOR FILING DATE: 2000-05-24
/ PRIOR APPLICATION NUMBER: 09/448,600
/ PRIOR FILING DATE: 1999-11-24
/ PRIOR APPLICATION NUMBER: 09/084,777
/ PRIOR FILING DATE: 1998-05-27
/ PRIOR APPLICATION NUMBER: 60/047,753
/ PRIOR FILING DATE: 1997-05-27
/ PRIOR APPLICATION NUMBER: 60/047,779
/ PRIOR FILING DATE: 1997-05-28
/ PRIOR APPLICATION NUMBER: 60/075,863
/ PRIOR FILING DATE: 1998-02-25
/ PRIOR APPLICATION NUMBER: 60/075,864
```

```
/ PRIOR FILING DATE: 1998-02-25
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 3888
/ TYPE: DNA
/ ORGANISM: Unknown Organism
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1555)..(1908)
/ NAME/KEY: CDS
/ LOCATION: (2149)..(2655)
/ OTHER INFORMATION: Description of Unknown Organism: Phaseolin
US-09-897-898-7

Alignment Scores:
Pred. No.: 1.47e-60 Length: 3888
Score: 482.00 Matches: 88
Percent Similarity: 89.38% Conservative: 13
Best Local Similarity: 77.88% Mismatches: 12
Query Match: 78.37% Indels: 0
DB: Gaps: 0

US-09-786-715-6 (1-120) x US-09-897-898-7 (1-3888)
QY 4 SerSerGluGluGlyGlnValIleSerCysHisThValGluGluTrpAsnAspGlnLeu 23
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 2317 GCTTCGGAAGAGACAAAGTATCGCTCCACACCGTTGAGACATGGAACGACGAGCTT 2376
QY 24 GlnYsGlyAsnGluSerLysLysLeuIleValIleValAspPheThrAlaSerTrpCysGly 43
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2377 CAGAAAGCTAATGAATCCAAACTCTTGCTGGTGATTTACGGCTCTTGCTGGA 2436
QY 44 ProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIle 63
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2437 CCGATGCGTTTCATCGCTCCATCTTCTTGCTGATTTGGCTAGAACTTCTTAACGTCCTT 2496
QY 64 PheLeuLysValAspValAspLysLysLysLysLysLysLysLysLysLysLysLysLys 83
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2497 TTCCTCAAGGTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2556
QY 84 MetProThrPheValPheValLysGluGlyThrLeuLeuAspLysValIleGlyAlaLys 103
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2557 ATGCCAACCTTCATGTTTGAAGGAGGAGATTTGGACAAAGTTGTGGAGCCAG 2616
QY 104 LysAspGluLeuGlnGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2617 AAAGATGAGCTTCAGTCTACATTCGCAACACTTGCGCT 2655

RESULT 5
US-09-878-574-3723
/ Sequence 3723, Application US/09878574
/ Patent No. US20020110548A1
/ GENERAL INFORMATION:
/ APPLICANT: BYRUM, Joseph R.
/ APPLICANT: Ia Rosa, Thomas J.
/ APPLICANT: Thompson, Michael D.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ FILE REFERENCE: 38-21(15401)B
/ CURRENT APPLICATION NUMBER: US/09/878,574
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 09/333,535
/ PRIOR FILING DATE: 1999-06-14
/ NUMBER OF SEQ ID NOS: 15775
/ SEQ ID NO 3723
/ LENGTH: 402
/ TYPE: DNA
/ ORGANISM: Glycine max
/ OTHER INFORMATION: Clone ID: LIB3028-006-Q1-B1-F8
US-09-878-574-3723
```

;; PRIOR FILING DATE: 1997-05-28
;; PRIOR APPLICATION NUMBER: 60/075,863
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/075,864
;; PRIOR FILING DATE: 1998-02-25
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 10
;; LENGTH: 3888
;; TYPE: DNA
;; ORGANISM: Unknown Organism
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1555)..(2250)
;; NAME/KEY: CDS
;; LOCATION: (2491)..(2655)
;; OTHER INFORMATION: Description of Unknown Organism: Phaseolin
;; OTHER INFORMATION: promoter-Trrh oleosin-phaseolin terminator
US-09-897-898-10

Alignment Scores:
Pred. No.: 5,26e-61 Length: 3888
Score: 485.00 Matches: 89
Percent Similarity: 88.70% Conservative: 13
Best Local Similarity: 77.39% Mismatches: 13
Query Match: 78.86% Indels: 0
Gaps: 0

US-09-786-715-6 (1-120) x US-09-897-898-10 (1-3888)

QY 4 SerSerGluglGlnGlnValIleSerCysHisThrValGluGluTrpPasnAspGlnLeu 23
Db 1558 GCTTCGGAAGAGCAAGTGTATGCGCTGCCACCGCTTGAGACATGGAACGACACTT 1617
QY 24 GlnTsgLysnGlnSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGly 43
Db 1618 CAGAGGCTATGATGATCAAAACCTTGTGTGCTGATTTACGCGCTTCTTGGTGGA 1677
QY 44 ProcysArpPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIle 63
Db 1678 CCATGTCGTTTCATCGCTCCATCTTGTGATTTGGCTAAGAACTTCCTAACGTGCTT 1737
QY 64 PheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAla 83
Db 1738 TTCTCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1797
QY 84 MetProthrPheValPheValLysGluGlyThrLeuLeuAspLysValValAlaLys 103
Db 1798 ATGCCAACCTTCATGTTTGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1857
QY 104 LysAspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAla 118
Db 1858 AAGATGAGCTTCAGTCTACCATTTGCCAAACACTTGCTATGGCG 1902

RESULT 2
US-09-938-842A-163
;; Sequence 163, Application US/09938842A
;; Patent No. US20020160378A1
;; GENERAL INFORMATION:
;; APPLICANT: Harper, Jeff
;; APPLICANT: Kieps, Joel
;; APPLICANT: Wang, Xun
;; APPLICANT: Zhu, Tong
;; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;; FILE REFERENCE: SCRIPI300-3
;; CURRENT APPLICATION NUMBER: US/09/938,842A
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: US 60/227,866
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: US 60/264,647
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: US 60/300,111

;; PRIOR FILING DATE: 2001-06-22
;; NUMBER OF SEQ ID NOS: 5379
;; SEQ ID NO 163
;; LENGTH: 345
;; TYPE: DNA
;; ORGANISM: Arabidopsis thaliana
US-09-938-842A-163

Alignment Scores:
Pred. No.: 4,05e-62 Length: 345
Score: 482.00 Matches: 88
Percent Similarity: 89.38% Conservative: 13
Best Local Similarity: 77.88% Mismatches: 12
Query Match: 78.37% Indels: 0
Gaps: 0

US-09-786-715-6 (1-120) x US-09-938-842A-163 (1-345)

QY 4 SerSerGluglGlnGlnValIleSerCysHisThrValGluGluTrpPasnAspGlnLeu 23
Db 4 GCTTCGGAAGAGCAAGTGTATGCGCTGCCACCGCTTGAGACATGGAACGACACTT 63
QY 24 GlnTsgLysnGlnSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGly 43
Db 64 CAGAGGCTATGATGATCAAAACCTTGTGTGCTGATTTACGCGCTTCTTGGTGGA 123
QY 44 ProcysArpPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIle 63
Db 124 CCATGTCGTTTCATCGCTCCATCTTGTGATTTGGCTAAGAACTTCCTAACGTGCTT 183
QY 64 PheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAla 83
Db 184 TTCTCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
QY 84 MetProthrPheValPheValLysGluGlyThrLeuLeuAspLysValValAlaLys 103
Db 244 ATGCCAACCTTCATGTTTGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 303
QY 104 LysAspGluLeuGlnGlnLysIleGlnLysHisValAla 116
Db 304 AAGATGAGCTTCAGTCTACCATTTGCCAAACACTTGCT 342

RESULT 3
US-09-897-898-5
;; Sequence 5, Application US/09897898
;; Patent No. US20020037303A1
;; GENERAL INFORMATION:
;; APPLICANT: DECKERS, HARM M.
;; APPLICANT: VAN ROOIJEN, GIJS
;; APPLICANT: BOOTHE, JOSEPH
;; APPLICANT: GOEL, JANIS
;; APPLICANT: MOLONEY, MAURICE M.
;; APPLICANT: DALMIA, BIPIN K.
;; TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
;; FILE REFERENCE: 034547/0104
;; CURRENT APPLICATION NUMBER: US/09/897,898
;; CURRENT FILING DATE: 2001-09-21
;; PRIOR APPLICATION NUMBER: 09/577,147
;; PRIOR FILING DATE: 2000-05-24
;; PRIOR APPLICATION NUMBER: 09/448,600
;; PRIOR FILING DATE: 1999-11-24
;; PRIOR APPLICATION NUMBER: 09/084,777
;; PRIOR FILING DATE: 1998-05-27
;; PRIOR APPLICATION NUMBER: 60/047,753
;; PRIOR FILING DATE: 1997-05-27
;; PRIOR APPLICATION NUMBER: 60/047,779
;; PRIOR FILING DATE: 1997-05-28
;; PRIOR APPLICATION NUMBER: 60/075,863
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/075,864
;; PRIOR FILING DATE: 1998-02-25
;; NUMBER OF SEQ ID NOS: 24

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 19:25:47 ; Search time 139.876 seconds
(without alignments)
1919.938 Million cell updates/sec

Title: US-09-786-715-6

Perfect score: 615

Sequence: 1 MAGSSEGVISCHTEWEN.....GAKKDELQKIQKHVASASA 120

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1504479 seqs, 118970152 residues

Total number of hits satisfying chosen parameters: 3008958

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q=/cg2_1/USPTO_pool/US09786715/runat_11082003_150515_6129/app_query.fasta_1.1052
-DB=Published_Applications_NA -QMT=fastap -SUFFIX=trpb -MIMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-FRAN=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pcr -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=local -OUTFMT=ptc -NORM=ext -HEARSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USBR=US0987615 @CGN 1.1.560 @runat_11082003_150515_6129
-NCPU=6 -ICPU=3 -NO.MARP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSFBLCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5
-FEAPOP=6 -FEAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1:	/cg2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2:	/cg2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3:	/cg2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4:	/cg2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5:	/cg2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6:	/cg2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cg2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8:	/cg2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9:	/cg2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10:	/cg2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11:	/cg2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12:	/cg2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:	/cg2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14:	/cg2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15:	/cg2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
16:	/cg2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
17:	/cg2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485	78.9	3888	9	US-09-897-898-10 Sequence 10, Appl

2	482	78.4	345	10	US-09-938-842A-163	Sequence 163, App
3	482	78.4	3129	9	US-09-897-898-5	Sequence 5, Appl
4	482	78.4	3888	9	US-09-897-898-7	Sequence 7, Appl
5	438	71.2	402	10	US-09-878-574-3723	Sequence 3723, Ap
6	424	68.9	392	10	US-09-878-574-104	Sequence 104, App
7	391	63.6	390	10	US-09-878-574-1462	Sequence 1462, Ap
8	387	62.9	540	12	US-10-349-782-12	Sequence 12, Appl
9	381.5	62.0	360	10	US-09-938-842A-164	Sequence 164, App
10	376.5	61.2	357	10	US-09-938-842A-1736	Sequence 1736, Ap
11	376.5	61.2	357	14	US-10-323-362-1	Sequence 1, Appl
12	368	59.8	393	12	US-10-091-841-5	Sequence 5, Appl
13	367	59.7	382	12	US-10-091-841-3	Sequence 3, Appl
14	361	58.7	369	12	US-10-194-885-8	Sequence 8, Appl
15	361	58.7	369	12	US-10-091-841-1	Sequence 1, Appl
16	358	58.2	659	12	US-10-349-782-9	Sequence 9, Appl
17	316	51.4	277	10	US-09-878-574-8135	Sequence 8135, Ap
18	300	48.8	260	10	US-09-878-574-12941	Sequence 12941, A
19	293	47.6	370	10	US-09-878-574-3169	Sequence 3169, Ap
20	289	47.0	268	10	US-09-878-574-5995	Sequence 5995, Ap
21	285.5	46.4	402	10	US-09-938-842A-225	Sequence 225, App
22	285.5	46.4	613	9	US-09-770-149-855	Sequence 855, App
23	283	46.0	270	10	US-09-878-574-13445	Sequence 13445, A
24	279	45.4	272	10	US-09-878-574-12181	Sequence 11, Appl
25	274	44.6	297	12	US-10-349-782-11	Sequence 11, Appl
26	272	44.2	456	10	US-09-924-035A-677	Sequence 677, App
27	256	41.6	350	9	US-09-923-876-1288	Sequence 1288, Ap
28	255	41.5	390	10	US-09-938-842A-2688	Sequence 2688, Ap
29	252	41.0	267	10	US-09-878-574-11337	Sequence 13337, A
30	237	38.5	261	10	US-09-878-574-7974	Sequence 7974, Ap
31	229	37.2	440	9	US-09-770-444-914	Sequence 914, App
32	226	36.7	357	10	US-09-938-842A-147	Sequence 147, App
33	222	36.1	301	9	US-09-815-343-76	Sequence 76, Appl
34	222	36.1	413	14	US-10-102-524-1396	Sequence 1396, Ap
35	222	36.1	418	10	US-09-796-692-3641	Sequence 3641, Ap
36	222	36.1	418	14	US-10-040-862-3641	Sequence 3641, Ap
37	222	36.1	464	10	US-09-998-598-1059	Sequence 1059, Ap
38	222	36.1	479	11	US-09-535-459-1145	Sequence 1145, Ap
39	222	36.1	536	14	US-10-066-543-65	Sequence 65, Appl
40	222	36.1	540	10	US-09-920-300A-1247	Sequence 1247, Ap
41	222	36.1	540	13	US-10-033-528-1247	Sequence 1247, Ap
42	222	36.1	557	10	US-09-884-441-88	Sequence 88, Appl
43	222	36.1	557	11	US-09-907-965-88	Sequence 88, Appl
44	222	36.1	557	14	US-10-198-053-88	Sequence 88, Appl
45	222	36.1	568	11	US-09-535-459-1139	Sequence 1139, Ap

ALIGNMENTS

RESULT 1
US-09-897-898-10
; Sequence 10, Application US/09897898
; Patent No. US20020037303A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.
; APPLICANT: VAN ROOIJEN, GIJS
; APPLICANT: BOOTHIE, JOSEPH
; APPLICANT: GOLL, JANIS
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
; FILE REFERENCE: 034547/0104
; CURRENT APPLICATION NUMBER: US/09/897,898
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/577,147
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/448,600
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/084,777
; PRIOR FILING DATE: 1998-05-27
; PRIOR APPLICATION NUMBER: 60/047,753
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: 60/047,779

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 18:47:50 ; Search time 1887.34 Seconds

(without alignments)
2644.453 Million cell updates/sec

Title: US-09-786-715-2

Perfect score: 637

Sequence: 1 MAEGGYIACKIDWEGQL.....GLSKILELSTTPATSTA 122

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+P2n.model -DEV=slp
-O=/cgn2.1/USPTO/US09786715/runat_11082003_150514_6035/app_query.fasta_1.1052
-DB=genEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=humana40.cdi -LIST=45
-DOCLALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09786715 -GCGN_1.1_5721 -ernat_11082003_150514_6035 -NCPU=6 -ICPU=3
-NO_MMAP -LARGOQUERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mnu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_nam:*
37: em_htg_vrl:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	385	60.4	345	8	AF483265 Populus t
2	377	59.2	664	8	AF323593 Prunus pe
3	376	59.0	345	6	AX505468 Sequence
4	376	59.0	480	8	AY088687 Arabidops
5	376	59.0	497	8	ATTTHIOARA
6	368	57.8	603	8	RCFHIORXN
7	354	55.6	665	8	AY170650
8	352	55.3	595	8	D87984
9	352	55.3	630	8	PSA310990
10	348.5	54.7	698	8	NTTRNA
11	348.5	54.4	590	8	AY088698
12	345.5	54.2	360	6	AX505469
13	345.5	54.2	360	8	BF004710
14	345.5	54.2	556	8	AK118542
15	343.5	53.9	641	8	AF051206
16	343	53.8	526	11	G73679
17	343	53.8	601	8	OS092541
18	343	53.8	686	6	E08194
19	343	53.8	687	8	RICHT
20	342.5	53.8	642	8	ATTTHRED1
21	342.5	53.8	784	8	AY271308
22	337	52.9	357	8	AY040028
23	337	52.9	528	8	ATTTHRED4
24	337	52.9	530	8	AK118035
25	337	52.9	560	8	AY087159
26	337	52.9	561	8	AF360227
27	335.5	52.7	653	6	AR016869
28	335.5	52.7	653	6	AR020895
29	335.5	52.7	653	6	AR027218
30	335.5	52.7	653	6	AR038505
31	335.5	52.7	653	6	AR064647
32	335.5	52.7	653	6	AR067572
33	335.5	52.7	653	6	I38524
34	335.5	52.7	653	6	I56999
35	335.5	52.7	653	6	I59865
36	335.5	52.7	653	6	I75192
37	334	52.4	593	8	PSA319808
38	330	51.8	582	3	AB061204
39	323	50.7	357	6	AX412276
40	323	50.7	357	6	AX412277
41	323	50.7	357	6	AX412278
42	323	50.7	357	6	AX412279
43	323	50.7	357	6	AX412473
44	323	50.7	357	6	AX412474
45	323	50.7	357	6	AX412566

ALIGNMENTS

RESULT 1

AF483265 345 bp mRNA linear PLN 01-APR-2002
LOCUS AF483265
DEFINITION Populus tremula x Populus tremuloides thioedoxin H mRNA, complete cds.
ACCESSION AF483265
VERSION AF483265.1 GI:19851971
KEYWORDS
SOURCE ORGANISM
Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE
AUTHORS Behm, M. and Jacquot, J.P.
TITLE Isolation and characterization of thioedoxin h from poplar xylem
JOURNAL Plant Physiol. Biochem. 38 (5), 363-369 (2000)
REFERENCE
AUTHORS Behm, M. and Jacquot, J.P.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-2002) Faculte des Sciences, Universite Henri Poincare, Bd des Aiguillettes, Vandoeuvre 54506, France
FEATURES
source
1..345
Location/Qualifiers
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
1..345
/codon_start=1
/product="thioedoxin H"
/protein_id="AAL99941.1"
/db_xref="GI:19851972"
/translation="MAEAGVIACTHVDVWKEHEKSGSKLIIVDFASWCPCK
IAPIFAELAKRPFVFLKVDVDELKAVAEEMVEMPFIFLKDGLYDKTGADKD
GLPTLVAKHNTA"
CDS
/codon_start=1
/product="thioedoxin H"
/protein_id="AAL99941.1"
/db_xref="GI:19851972"
/translation="MAEAGVIACTHVDVWKEHEKSGSKLIIVDFASWCPCK
IAPIFAELAKRPFVFLKVDVDELKAVAEEMVEMPFIFLKDGLYDKTGADKD
GLPTLVAKHNTA"
BASE COUNT 101 a 61 c 95 g 88 t
ORIGIN
Alignment Scores:
Pred. No.: 1,22e-35 Length: 345
Score: 385.00 Matches: 70
Percent Similarity: 78.85% Conservative: 12
Best Local Similarity: 67.31% Mismatches: 22
Query Match: 60.44% Indels: 0
Gaps: 0
DB: 8
US-09-786-715-2 (1-122) x AF483265 (1-345)
QY 1 MetAlaGluGluGlyGlnValIleAlaCysHisLysIleAspGluTrpGluGlnLeu 20
DB 1 ATGGCCGAGAGAGACAGATTATTCCTGCCACACAGTGTGATCTGGAAGAGCATTTTC 60
QY 21 GlyLysTrpLysAspSerGluLysLeuValValValAspPheThrAlaSerTrpCysGly 40
DB 61 GAAAGGAAAGAGGCTCTGAGAAAGCATGTGCTGATTTTACTGCTTCATGCTGCCA 120
QY 41 ProCysArgAlaIleAlaProTrpPheThrGluLeuAlaLysAsnAsnProAsnValAla 60
DB 121 CCATGTAAATGATTTGCTCCAAATCTCGCCAGTGTGGCGAAGAGTTTCCCAATGTCACA 180
QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
DB 181 TTCTTAAGGTGGATGGATGATGAAAGCTGTGCTGAGAGTGGAAATGTGAGCGCA 240
QY 81 MetProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValAlaAsp 100
DB 241 ATGCCCAACTTTTATTTTCCGAAAGATGGAATTTAGTGACAAACTGTGGCTGCTGAT 300
QY 101 LysValGlyLeu 104
DB 301 AAAGATGCCTG 312
RESULT 2
AF323593

AF323593 664 bp mRNA linear PLN 02-NOV-2001
LOCUS AF323593
DEFINITION Prunus persica thioedoxin H mRNA, complete cds.
ACCESSION AF323593
VERSION AF323593.1 GI:16588842
KEYWORDS
SOURCE ORGANISM
Prunus persica (peach)
Prunus persica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE
AUTHORS Callahan, A.M., Morgens, P.H. and Cohen, R.A.
TITLE Isolation and initial characterization of cDNAs for mRNAs regulated during peach fruit development
JOURNAL J. Am. Soc. Hortic. Sci. 118, 531-537 (1993)
REFERENCE
AUTHORS Callahan, A.M., Dunn, L.L. and Cohen, R.A.
TITLE Regulation of peach gene expression in a peach/almond hybrid
JOURNAL Unpublished
REFERENCE
AUTHORS Callahan, A.M., Dunn, L.L. and Cohen, R.A.
TITLE Direct Submission
JOURNAL Submitted (22-NOV-2000) USDA-ARS, Appalachian Fruit Research Station, 45 Wiltshire Rd., Kearneysville, WV 25430, USA
FEATURES
source
1..664
Location/Qualifiers
/organism="Prunus persica"
/mol_type="mRNA"
/cultiar="B612615"
/db_xref="taxon:3760"
/clone="pch306c"
/tissue="peach fruit"
71..481
/codon_start=1
/product="thioedoxin H"
/protein_id="AAL26915.1"
/db_xref="GI:16588843"
/translation="MAEENOVICHTTQAEQOLHKNENKLLVVDFTASWCPCK
IAPIFAELAKRPFVFLKVDVDELTVSEEMVEMPFIFLKEKIVDKYVGAARD
ELQIKVAKHVAANAASATASATATATATATA"
CDS
/codon_start=1
/product="thioedoxin H"
/protein_id="AAL26915.1"
/db_xref="GI:16588843"
/translation="MAEENOVICHTTQAEQOLHKNENKLLVVDFTASWCPCK
IAPIFAELAKRPFVFLKVDVDELTVSEEMVEMPFIFLKEKIVDKYVGAARD
ELQIKVAKHVAANAASATASATATATATATA"
BASE COUNT 182 a 147 c 161 g 174 t
ORIGIN
Alignment Scores:
Pred. No.: 2.19e-34 Length: 664
Score: 377.00 Matches: 74
Percent Similarity: 68.18% Conservative: 16
Best Local Similarity: 56.06% Mismatches: 32
Query Match: 59.18% Indels: 10
Gaps: 1
DB: 8
US-09-786-715-2 (1-122) x AF323593 (1-664)
QY 1 MetAlaGluGluGlyGlnValIleAlaCysHisLysIleAspGluTrpGluGlnLeu 20
DB 71 ATGGCCGAGAGAAATGATGATGCTGCCACACTACTCAACCTGGGAAGAGAGCTTC 130
QY 21 GlyLysTrpLysAspSerGluLysLeuValValValAspPheThrAlaSerTrpCysGly 40
DB 131 CATTAAGGAAAGACAGAACAAAGATGCTGCTGATTTTCACGGCTTCGCTGTGCA 190
QY 41 ProCysArgAlaIleAlaProTrpPheThrGluLeuAlaLysAsnAsnProAsnValAla 60
DB 191 CCCTGCCGGGTATGTCGCCCAATCTTGGCGAGTGTGCTAAAGAACCCAGAAAGTGAAG 250
QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
DB 251 TTCTTAAGGTGGATGATGATGAAAGCTGTGCTGAGAGTGGAAATGTGAGCGCA 310
QY 81 MetProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValAlaAsp 100
DB 311 ATGCTACTCTCTCTCTCTCAAGAGAGGCAAGATAGTGACAAAGTGTGGTGCACAG 370

[illegible]

ACCESSION	AY086867
VERSION	AY086867.1
KEYWORDS	GI:21407461
SOURCE	EIL_CDNA.
ORGANISM	Arabidopsis thaliana (thale cress)
	Arabidopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE	1 (bases 1 to 480) Haas,B.J., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salberg,S.L. Full-length messenger RNA sequences greatly improve genome annotation
TITLE	Genome Biol. 3 (6), RESEARCH0029 (2002)
JOURNAL	Medline
PUBMED	22088475
REFERENCE	2 (bases 1 to 480) Brover,V.Y., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
AUTHORS	Full-length cDNA from Arabidopsis thaliana
TITLE	Unpublished
JOURNAL	3 (bases 1 to 480)
REFERENCE	Brover,V.Y., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
AUTHORS	Direct Submission
TITLE	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
JOURNAL	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the WS or Luer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genet carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
FEATURES	Location/Qualifiers
source	1..480 /organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" /clone="9189" 13..357 /codon_start=1 /product="chlorodoxin b" /protein_id="AA067008.1" /db_xref="GI:21617938" /translation="MASEEIVAGCHVETWNEQLOKANESEKLTVVDFTASMGCPDCT FIAPGFADLAKRLPNVLFLKVDTELSVASDWAIOAMPPTFMLEKGLIDKKVGAKAK DELQSTIAKHIA"
CDS	BASE COUNT 124 a 93 c 111 g 152 t ORIGIN
Alignment Scores:	
Pred. No.:	1,96e-34 Length: 480
Score:	376.00 Matches: 71
Percent Similarity:	77.57% Conservative: 12
Best Local Similarity:	66.36% Mismatch: 24
Query Match:	59.03% Indels: 0
DB:	Gaps: 0
US-09-786-715-2 (1-122) x AY086867 (1-480)	
OY	2 AAlagctugtcgtgacgaagcattgcctccaccacccgttgacatcgaaacgacctttag 78
DB	19 TCgGAAGAAGGACCAAGTGCCTCCACCACCGCTTGACATCGAAGCAGACTTTGAC 78

OY	22	ysrTrpLysaspSerGlnLysLeuValValValaspPheThrAlaSerTrpCysGlyPro	41
		
Db	79	AAGCGTAATGATCCAAACACTTGTGTGGTTGATTTCACGCGCTTCTGTGTGTGACCA	138
OY	42	CysaRgaLalIealaProTyrPheThrGlnLeuAlaLysAsnAsnProAsnValaPhe	61
		
Db	139	TGTGCTTTCATCGCCCACTCTTTCCTATTTGGCTAAGAAACTCTTAACCTGCCTTTC	198
OY	62	LeuLysValaspValaspGlnLeuAsnSerValAlaSerLysTrpGlnIleAsnIleMet	81
		
Db	199	CTCAAGGTGTAAGTGAATTCGAAGTCGGTGGCAAGATTTGGCGATACAGCGATG	258
OY	82	ProThrPheValPheLeuLysLysGlyLysIleIleGlnLysIleValAlaLaspAsp	101
		
Db	259	CCAACCTTCATGTTTTCGAAGGAAGGAATTTGGACAAAGTTGTGGACCAAGAA	318
OY	102	ValGlyLeuSerLysLysIle	108
		
Db	319	GATGAGCTCAAGTCAACCATT	339

RESULT 5			
ATTHIOARA			
LOCUS	ATTHIOARA	497 bp	mRNA
DEFINITION	A. thaliana mRNA for thioredoxin H.		
ACCESSION	Z14084		linear
VERSION	Z14084.1	GI:16551	
KEYWORDS	Thioredoxin H.		
SOURCE	Arabidopsis thaliana	(thale cress)	
ORGANISM	Arabidopsis thaliana		

REFERENCE	1 (bases 1 to 497)
AUTHORS	Rivera-Madrid, R., Marinho, P., Brugioud, C., Chartier, Y. and Meyer, Y.
TITLE	Nucleotide sequence of a cDNA clone encoding an Arabidopsis thaliana thioredoxin h
JOURNAL	Plant Physiol. 102 (1), 327-328 (1993)
MEDLINE	94151431
PUBMED	8108503
REFERENCE	2 (bases 1 to 497)
AUTHORS	Meyer, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-1992) Yves Meyer PhD, Laboratoire de Physiologie végétale, Université de Perpignan, Av de Villeneuve 52, Perpignan 66860, FRANCE

CDs	Location/Qualifiers
1. .497	/organism="Arabidopsis thaliana"
	/mol_type="rRNA"
	/db_xref="taxon:3702"
30. .374	

```

CDS
30..374
/codon_start=1
/product="phloretodoxin H"
/protein_id="CAA78462.1"
/db_xref="GI:16553"
/db_xref="SMSS-PROT:P29448"
/translacion="MASEGVYCHIVETYNQLOKANESKTLVYVDFTSWCGPCCI
FIAPFADLARKLPNVLFLEKVDDELKSVASDWAIAQAPTEFLKEGRILDKVYGAKR
DELSTIARKHLA"
BASE COUNT
135 a 94 c 116 g 152 t
ORIGIN

```

Alignment Scores:	
Pred. NO.:	2.04e-34
Score:	376.00
Percent Similarity:	77.57%
Best Local Similarity:	66.36%
Query Match:	59.03%
DB:	8
Gaps:	0
length:	497
Matches:	71
Conservative:	12
Mismatches:	24
Indels:	0
Gaps:	0

US-09-786-715-2 (1-122) x ATTIOARA (1-497)

[illegible]

RESULT 6			
RCTHIORXN			
LOCUS	RCTHIORXN	603 bp	mRNA
DEFINITION	R.cthiorn mRNA for thioredoxin.		
ACCESSION	Z70677		
VERSION	Z70677.1 GI:1255953		
KEYWORDS	thioredoxin.		
SOURCE	Ricinus communis (castor bean)		
ORGANISM	Ricinus communis		
		linear	PLN 04-APR-1996

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 603)
Szedekenyi,J., Dolgener,E. and Schobert,C.
cDNA expressed in Ricinus cotyledons
unpublished
2 (bases 1 to 603)
Dolgener,E.
Direct Submission
Submitted (04-APR-1996) Dolgener E., University of Bayreuth,
Department of Plant Physiology, Universitaetsstr.30, Bayreuth,
Germany, 95440

```
FEATURES
source
location/Qualifiers
1..603
/organism="Ricinus communis"
/mol_type="mrna"
/cultivar="Sanguineus"
/db_xref="taxon:3988"
```

```

CDS
/db_xref="taxon:3988"
/clone="PEDRH018"
/tissue_type="cotyledon"
/clone_lib="lambda Excell"
/dev_stage="seedling"
23..379
/codon_start=1
/product="Chlorodoxin"
/protein_id="CAA94534.1"
/db_xref="GI:1255954"
/db_xref="SPTRMEMB:Q43656"

```

BASE COUNT	179 a	101 c	157 g	166 t
ORIGIN	FIAAFIAELAKLNNVPEFLKVDDELKIVAHENMAVESNPPTMFLKEGKIMDKVYGAKK DELOQTAKKHATATST"			
Alignment Scores:	2.16e-33 Length: 603			
Aligned. NO.:				

Best Local Similarity: 60.18%

Query Match: 57.77% Indels: 0
 DB: 8 Gaps: 0
 US-09-786-715-2 (1-122) x RCHTHORXN (1-603)

QY 2 Aaagiugluglvglnvalillealacyshtslsyleaspglutrpgluglvglnleugly 21
 DB 29 GCAGAGAAGGCAAGTATCGCGTGCACACTGTGAGGATGAGATGAGCAATGTGCG 88
 QY 22 LysTrpLysAspSerGclLysLeuValValAlaAspPheThrAlaSerTrpCysGly 41
 DB 89 AAGGGAATGATACCAAGGAGTGCCTGTGATTACGCTTCATGCGTGCAGCA 148
 QY 42 CysarGalAlaIleAlaProTyrPheThrGluLeuAlaLysAsnProAsnValAlaPhe 61
 DB 149 TGCCCTTCATTCGCTCCCTTCCTTGGCTGAGCTGCCAAGAACTCCCAATGTTCCTTC 208
 QY 62 LeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAlaMet 81
 DB 209 CTGAAGTGTGATGTGATGAACTGAAAGACTGTGCTCAAGAGTGGCGTGTGAGTCATG 268
 QY 82 ProThrPheValPheLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 101
 DB 269 CCACCTTATGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 328
 QY 102 ValGlyLeuSerLysLysLysLysLysLysLysLysLysLysLysLysLysLys 114
 DB 329 GACGACTGCACAACTATACGCAACACATGCTGCTACT 367

RESULT 7
 LOCUS AY170650 665 bp mRNA linear PIN 02-JAN-2003
 DEFINITION Pisum sativum clone 3 thioedoxin h mRNA, complete cds.
 ACCESSION AY170650.1 GI:27466893
 VERSION AY170650.1
 KEYWORDS
 SOURCE
 ORGANISM

Pisum sativum (pea)
 Pisum sativum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
 Pisum.

REFERENCE
 AUTHORS Montichard, F., Renard, M., Duval, F.D. and Macherel, D.
 TITLE Expression of the NADP-thioedoxin reductase/thioedoxins h system
 JOURNAL during germination of seeds of Pisum sativum L
 REFERENCE 2 (bases 1 to 665)
 AUTHORS Montichard, F., Renard, M., Duval, F.D. and Macherel, D.
 TITLE Direct Submission
 JOURNAL Submitted (30-OCT-2002) UMR 1191 Physiologie Moléculaire des
 Semences, UFR Sciences, 16 bd Lavoisier, Angers 49045, France

FEATURES
 source
 1..665
 location/Qualifiers

CDS
 74..415
 /note="ex h"
 /codon_start=1
 /product="Chloredoxin h"
 /protein_id="AA012854.1"
 /db_xref="GI:27466894"
 /translation="MAEGQYIVCHTVDAMKEQLEKASKKLLIVDTASMGCPGRF
 IAPILAIATAKRLIVTFLKVDVDELKTVSEMGIEAMPTFLKNGELVDKVGAKKE
 ELQKIDHHA"

BASE COUNT 220 a 85 c 164 g 196 t
 ORIGIN

Alignment Scores: 1.01e-31 Length: 665
 Pred. No.: 354.00 Matches: 67
 Score:

Percent Similarity: 75.93% Conservative: 15
 Best Local Similarity: 62.04% Mismatches: 26
 Query Match: 55.57% Indels: 0
 DB: 8 Gaps: 0
 US-09-786-715-2 (1-122) x AY170650 (1-665)

QY 1 MetAaagiugluglvglnvalillealacyshtslsyleaspglutrpgluglvglnleu 20
 DB 74 ATGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 133
 QY 21 GlyLysTrpLysAspSerGclLysLeuValValAlaAspPheThrAlaSerTrpCysGly 40
 DB 134 GAGGAAGGAGAAAGCCCTCAAGAAAGTGTGATGATGATGATGATGATGATGATGATGAT 193
 QY 41 ProCysarGalAlaIleAlaProTyrPheThrGluLeuAlaLysAsnProAsnValAla 60
 DB 194 CCATCCCGTTTATTCGCCCCCAATTTTGGCAGGAGTGTGTAACCTTACACATGCTACT 253
 QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
 DB 254 TTCCTTAAGTGTGAGTGTGATGAAAGACTGTTCCGAGAGTGGGAGGAAATTCAGCT 313
 QY 81 MetProThrPheValPheLeuLysLysLysLysLysLysLysLysLysLysLysLys 100
 DB 314 ATGCCACATTCCTTCTGTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 373
 QY 101 LysValGlyLeuSerLysLysLysLysLysLysLysLysLysLysLysLysLys 108
 DB 374 AAGGAGAGCTGCAATTCGAAATTT 397

RESULT 8
 LOCUS D87984 595 bp mRNA linear PIN 07-FEB-1999
 DEFINITION Fagopyrum esculentum mRNA for thioedoxin, complete cds.
 ACCESSION D87984
 VERSION D87984.1 GI:1620904
 KEYWORDS
 SOURCE
 ORGANISM

Fagopyrum esculentum (common buckwheat)
 Fagopyrum esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Polygonaceae; Fagopyrum.

REFERENCE
 AUTHORS Fujino, K., Funatsuki, H. and Kikuta, Y.
 TITLE buckwheat cDNA from immature seeds
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 595)
 AUTHORS Fujino, K.
 TITLE Direct Submission
 JOURNAL Submitted (24-SEP-1996) Kaizen Fujino, Hokkaido University, Faculty
 of Agriculture, Kita 9 Nishi 9, Kita-ku, Sapporo, Hokkaido 060,
 Japan (E-mail: kaizen@2.nines.hokudai.ac.jp, Tel: 011-706-2482,
 Fax: 011-706-2471)

FEATURES
 source
 1..595
 location/Qualifiers

CDS
 86..436
 /codon_start=1
 /product="thioedoxin"
 /protein_id="BA013524.1"
 /db_xref="GI:1620905"
 /translation="MAEAGYIACHTVOENNEKFOKANDSGKLIIVDTASMGCPGRV
 ITPYSELAKKFPYVAFKFDVDDDKVAEEYKVAEMSPFVILKGOVERIVGARKD
 ELKIKIVHAPITA"

BASE COUNT 170 a 107 c 157 g 161 t
 ORIGIN

Alignment Scores: 1.51e-31 Length: 595
 Pred. No.: 151.00 Matches: 67
 Score:

Score: 352.00 Matches: 66
 Percent Similarity: 75.93% Conservative: 16
 Best Local Similarity: 61.11% Mismatches: 26
 Query Match: 55.26% Indels: 0
 DB: 8 Gaps: 0

US-09-786-715-2 (1-122) x D87984 (1-595)

QY 1 MetAlaGluGluGlyGlnValIleAlaCysHisLysLleAspGluTrpGluGlnLeu 20
 Db 86 ATGGCGAAGACACACAGTATGCGATGCCACCGGTCCAGAGAGTGGAACGAAAGTTC 145
 QY 21 GlyLysTrpLysAspSerGluLysLeuValValAlaAspPheThrAlaSerTrpCysGly 40
 Db 146 CAGAAAGCCAGAGATTCGCCCAATTCATGTCATCATTCATCCGATCATGTCGGGT 205
 QY 41 ProCysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAla 60
 Db 206 CCTCGCCGCGTCAATCACTCCGTCGTGACGTCGCCAAGAGTTTCCTCATGTGGCC 265
 QY 61 PheLeuLysValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
 Db 266 TTCTTCAAGTGAATGTTGATTTGAAGAGATGTCCTCAGCAATACAGGTGGAGCA 325
 QY 81 MetProThrPheValPheLeuLysGlyLysIleIleGluLysIleValAlaAsp 100
 Db 326 ATGCCGAGCTTGTATTACTGAAGAAGGCGCAGAGAGTTGAAGATTTGGGTGCCAGG 385
 QY 101 LysValGlyLeuSerLysLysIle 108
 Db 386 AAGGACGAACTCCTTCATAGATA 409

RESULT 9

PSA310990 630 bp mRNA linear PLN 12-APR-2001
 LOCUS Pisum sativum mRNA for thioresdoxin h (trhx gene).
 DEFINITION AJ310990.1 GI:13624883
 VERSION thioresdoxin h; trhx gene.
 KEYWORDS Pisum sativum (pea)
 SOURCE Pisum sativum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.

REFERENCE 1
 AUTHORS Traverso, J.A.
 JOURNAL Thesis (2001). Department of Bioquímica, Biología Celular y Molecular de Plantas, Estación Experimental del Zaidin (C.S.I.C.), Granada, Spain

REFERENCE 2
 AUTHORS Traverso, J.A., Cazalis, R., Sahrawy, M., Lopez-Gorge, J. and Chueca, A.
 JOURNAL Sequencing, cloning and expression of Pisum sativum thioresdoxin h unpublished
 TITLE 3 (bases 1 to 630)
 AUTHORS Traverso, J.A.
 JOURNAL Direct Submission
 TITLE Submitted (11-APR-2001) Traverso J.A., Biología Celular y Molecular de plantas, Estación Experimental del Zaidin (CSIC), Profesor Albarreda 1, Granada, 18008, SPAIN

FEATURES
 source 1. 630
 /organism="Pisum sativum"
 /mol_type="mRNA"
 /variety="Lincoln"
 /db_xref="taxon:3888"
 /tissue_type="Leaves"
 1. 630
 /gene="trhx"
 35. 398
 /gene="trhx"
 /function="Unknown"
 /codon_start=1

/evidence=experimental
 /product="thioresdoxin h"
 /protein_id="CAC36986.1"
 /db_xref="GI:13624884"
 /translation="MAGSSEGGVISHSVANDNDLHRENSKLLIVDFTRSKCP
 CRFIAFLGLAKFTNVIPLKVDLKSADMDVAEAPTEFVKEETILGKVVGA
 KKELOQTIERHVAASSNA"
 398. .609
 /gene="trhx"
 /gene="trhx"
 609

3' UTR
 polyA_site
 BASE COUNT 195 a 95 c 141 g 199 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1 61e-31 Length: 630
 Score: 352.00 Matches: 66
 Percent Similarity: 74.77% Conservative: 14
 Best Local Similarity: 61.68% Mismatches: 27
 Query Match: 55.26% Indels: 0
 DB: 8 Gaps: 0

US-09-786-715-2 (1-122) x PSA310990 (1-630)

QY 2 AlaGluGluGlyGlnValIleAlaCysHisLysLleAspGluTrpGluGlnLeuGly 21
 Db 48 TCAGAGAGGAGACAGATTATCAGCTGCACAGCGTTGATCATGAGCAATATCCTTAC 107
 QY 22 LysTrpLysAspSerGluLysLeuValValAlaAspPheThrAlaSerTrpCysGlyPro 41
 Db 108 AGAGCAATCAATCCAGAAACGATGTTGTGACCTTCTCTTGTGTGGACCA 167
 QY 42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAlaPhe 61
 Db 168 TGCCGTTTCATTGACCATTCCTTGGTGAATGGCTACAGAAATGTCATATTC 227
 QY 62 LeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAlaMet 81
 Db 228 CTTAAGGTGACGCGAGCAACTAAGCTGTGCTCAGATATGGCGTGTGAGGCTATG 287
 QY 82 ProThrPheValPheLeuLysGlyLysIleIleGluLysIleValAlaAspLys 101
 Db 288 CCAACATTTGTTGTGAAAGAAAGCAACTTTGGCAAAAGTGTGGAGCAAAAGAA 347
 QY 102 ValGlyLeuSerLysLysIle 108
 Db 348 GAAGAACTGCACGACGACATTT 368

RESULT 10

LOCUS NTTRNA 698 bp mRNA linear PLN 15-FEB-1994
 DEFINITION N. tabacum mRNA for thioresdoxin.
 ACCESSION X58527.1 GI:20046
 VERSION X58527.1 GI:20046
 KEYWORDS thioresdoxin.
 SOURCE Nicotiana tabacum (common tobacco)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE 1
 AUTHORS Marty, I. and Meyer, Y.
 JOURNAL Nucleotide sequence of a cDNA encoding a tobacco thioresdoxin
 TITLE Plant Mol. Biol. 17 (1), 143-147 (1991)
 MEDLINE 91329721
 PUBMED 1868216

REFERENCE 2 (bases 1 to 698)
 AUTHORS Brugidou, C., Marty, I., Chartier, Y. and Meyer, Y.
 JOURNAL The Nicotiana tabacum genome encodes two cytoplasmic thioresdoxin genes which are differentially expressed
 TITLE Mol. Gen. Genet. 238 (1-2), 285-293 (1993)
 MEDLINE 93241165
 PUBMED 8479434

REFERENCE	3 (bases 1 to 698)
AUTHORS	Meyer, Y.
TITLE	Direct Submission
JOURNAL	Submitted (14-FEB-1991) Y. Meyer, Laboratoire de Physiologie et Biologie, Moleculaire Vegetale, Universite av de Villeneuve, 66860 Perpignan, France
COMMENT	Gene product is probably cytoplasmic.
FEATURES	Location/Qualifiers
source	1..698
	/organism="Nicotiana tabacum"
	/mol_type="mRNA"
	/strain="white Burley"
	/db_xref="taxon:4097"
	/clone_lib="plasmid PR219"
	/dev_stage="in vitro cells"
mrna	1..698
	/evidence=experimental
CDS	79..459
	/codon_start=1
	/product="thioredoxin"
	/protein_id="CAA1415.1"
	/db_xref="GI:20047"
	/db_xref="SWISS-PROT:P29449"
	/translation="MAANDATSEEGVFGCHKVEENNEYFKKGVETKKLVVDFTASWCGCKRIEPIADIARKMPHIVFLKVDVDELKTVSAEWSVEAPTEFVIDGKEVDPRVCGAKKEELQOTIVKHAAPATVZA"
polya_signal	468..473
polya_signal	511..517
polya_site	682
BASE COUNT	192 a 117 c 164 g 225 t
ORIGIN	
Alignment Scores:	
Pred. NO.:	4.62e-31
Score:	348.50
Percent Similarity:	72.73%
Best Local Similarity:	53.72%
Query Match:	54.71%
DB:	8
	gaps: 1
US-09-786-715-2 (1-122) x NTTRNA (1-698)	
OY	2
Db	103
OY	22
Db	163
OY	42
Db	223
OY	62
Db	283
OY	82
Db	343
OY	102
Db	403
OY	122
Db	454
RESULT 11	
LOCUS	AY088698
	590 bp
	mrna
	linear
	PLN 14-APR-2003

DEFINITION	Arabidopsis thaliana clone 9219 mRNA, complete sequence.
ACCESSION	AY088698
VERSION	AY088698.1
KEYWORDS	GI:21407472
SOURCE	FLI_CDNA.
ORGANISM	Arabidopsis thaliana (thale cress)
REFERENCE	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 590) Haas,B.J., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salberg,S.L.
TITLE	Full-length messenger RNA sequences greatly improve genome annotation
JOURNAL	Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE	22088475
PUBMED	12093376
REFERENCE	2 (bases 1 to 590) Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
TITLE	Full-length cDNA from Arabidopsis thaliana
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 590) Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
AUTHORS	Direct Submission
JOURNAL	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
COMMENT	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or later ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
FEATURES	Location/Qualifiers
SOURCE	1..590 /organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" /clone="9219"
CDS	52..411 /codon_start=1 /product="chlorodoxin" /protein_id="AA067018.1" /db_xref="GI:21617968" /translation="MAAEAGYVSCITNDWTVYDLDAKESNKIIVIDFATSKPPRCRMIATIFNDLAKRWFSSAIFFEVVDVDELOSVAKEGVEMAPTEVFIKGEVYDKLVGNM KEDLQATIVKRTGVTTA"
BASE COUNT	173 a 92 c 142 g 183 t
ORIGIN	
Alignment Scores:	
Pred. No.:	6,48e-31 Length: 590
Score:	346.50 Matches: 68
Percent Similarity:	74.36% Conservative: 19
Best local Similarity:	58.12% Mismatches: 29
Query Match:	54.40% Indels: 1
DB:	8 Gaps: 1
OS	US-09-786-715-2 (1-122) x AY088698 (1-590)
2	AlaGluGluGluGluGluValIleAlaCysHisLysIleAspGluTrpGluGluGlnLeuGly 21

```

Db      58 GCAGAGAGGCTCACTGATTAAGTTCACACGACGATGATGACCTGTCACACTGAT 117
Qy      22 LysTrpLysAspSerGluLysLeuValValValAspPheThrAlaSerTrpCysGlyPro 41
Db      118 AAGGCAAGAAACACACAGCAGTGCATGATGATGATTTACCTCCTTCATGCTCCACCA 177
Qy      42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAla--- 60
Db      178 TGCCGATGATGCTCCCAATTTTCACAGCATTTGCCACAGAACTTCATGTCACAGTGCATC 237
Qy      61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
Db      238 TTCTTCAAGGTGATGTGATTAAGTTCACAGAGTGTCTAAGAGTTGGTGGAGGCA 297
Qy      81 MetProThrPheValPheLeuLysGlyLysIleIleGluLysIleValAlaGlyAlaAsp 100
Db      298 ATGCCAACCCTTTGTGTTTCATTAAGCCGGCGAAGTTGTGATTAAGCTCGTTGGTGGCAAT 357
Qy      101 LysValGlyLeuSerLysLysIleLeuGluLeuSerGlyThrThrProAla 117
Db      358 AAGAGATCTTCAGCGCAAAATATGAGCATACTGTGTACACTGGC 408

RESULT 12
LOCUS      AX505469                360 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 164 from Patent WO0216555.
ACCESSION  AX505469
VERSION     AX505469.1  GI:23386706
KEYWORDS
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE   1
AUTHORS     Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
TITLE       Stress-regulated genes of plants, transgenic plants containing
            same, and methods of use
            Patent: WO 021655-A 164 28-FEB-2002;
            The Scripps Research Institute (US) ; Syngenta Participations AG
            (CH)
FEATURES
    source          1..360
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3702"
BASE COUNT      101 a      64 c      95 g      100 t
ORIGIN
Alignment Scores:
Pred. No.:      4..77e-31      Length:      360
Score:          345.50      Matches:      68
Percent Similarity: 73.50%      Conservative: 18
Best Local Similarity: 58.12%      Mismatches: 30
Query Match:    54.24%      Indels:      1
DB:             6      Gaps:      1

US-09-786-715-2 (1-122) x AX505469 (1-360)
Qy      2 AtAgUGUGUGlGlnValIleAlaCysHISLysIleAspGluTrpGluGlnLeuGly 21
Db      7 GCAGAGAGGCTCACTGATTAAGTTCACACGACGATGATGACCTGTCACACTGAT 66
Qy      22 LysTrpLysAspSerGluLysLeuValValValAspPheThrAlaSerTrpCysGlyPro 41
Db      67 AAGGCAAGAAACACACAGCAGTGCATGATGATGATTTACCTCCTTCATGCTCCACCA 126
Qy      42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAla--- 60
Db      127 TGCCGATGATGCTCCCAATTTTCACAGCATTTGCCACAGAACTTCATGTCACAGTGCATC 186
Qy      61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80

```

```

Db      187 TTCTTCAAGGTGATGTGATTAAGTTCACAGAGTGTGCTAAGAGTTGGTGGAGGCA 246
Qy      81 MetProThrPheValPheLeuLysGlyLysIleIleGluLysIleValAlaGlyAlaAsp 100
Db      247 ATGCCAACCCTTTGTGTTTCATTAAGCCGGCGAAGTTGTGATTAAGCTCGTTGGTGGCAAT 306
Qy      101 LysValGlyLeuSerLysLysIleLeuGluLeuSerGlyThrThrProAla 117
Db      307 AAGAGATCTTCAGCGCAAAATATGAGCATACTGTGTACACTGGC 357

RESULT 13
LOCUS      BT004710                360 bp      mRNA      linear      PLN 19-FEB-2003
DEFINITION Arabidopsis thaliana Atlg19730 gene, complete cds.
ACCESSION  BT004710
VERSION     BT004710.1  GI:28416850
KEYWORDS
SOURCE      FLI_CDNA.
            Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE   1 (bases 1 to 360)
AUTHORS     Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P.,
            Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
            Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
            Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
            Oudera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
            Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
            Yu, G., Yuan, S., Shinzaki, K., Davis, R.W., Theologis, A. and
            Ecker, J.R.
TITLE       Arabidopsis ORF clones
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 360)
AUTHORS     Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P.,
            Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
            Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
            Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
            Oudera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
            Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
            Yu, G., Yuan, S., Shinzaki, K., Davis, R.W., Theologis, A. and
            Ecker, J.R.
TITLE       Direct Submission
JOURNAL     Submitted (19-FEB-2003) Salk Institute Genomic Analysis Laboratory
            (SIGAL), Plant Biology Laboratory, The Salk Institute for
            Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
            USA
COMMENT
            RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RFL CDNA's (RFL CDNA : 'RIKEN
            Arabidopsis Full-length CDNA') : Seki, M., Narusaka, M., Ishida, J.,
            Hayashizaki, Y. and Shinzaki, K.

            The Salk, Stanford, PGEC (SSP) Consortium members constructed and
            sequenced the PUNT (ORF) clones using the RFL CDNA's: Cheuk, R.,
            Chen, H., Kim, C.J., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M.,
            Dale, J.M., Hsuan, V.W., Jones, T., Karlin-Neumann, G., Lam, B.,
            Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Oudera, C.S., Palm, C.J.,
            Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,
            Yamada, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A., and
            Ecker, J.R.

            Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
            this work. Shinzaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
            contributed equally to this work as PIs.

FEATURES
    source          1..360
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /chromosome="1"
                     /clone="U61017"
                     /note="This clone is in PUNT 51

```


CDs	ecotype: Columbia"	1. .360	/note="putative thioredoxin"	/codon_start=1	/product="Atlg19730"	/protein_id="AA042956.1"	/db_xref="gi:28416851"	/translation="MAEEGVIGCHTNDWTVOLDAKESNKIIVIDTASMPPCR MIAITFDLAKRFMSAIFFRVYDVDELSVAKEGVEMFLFVITAKEGVYDKLVGN KEDLQAIIVKHTGVTA
BASE COUNT	101 a	64 c	95 g	100 t				
ORIGIN								
Alignment Scores:								
Pred. No.:	4.77e-31	Length:	360					
Score:	345.50	Matches:	68					
Percent Similarity:	73.50%	Conservative:	18					
Best local Similarity:	58.12%	Mismatches:	30					
Query Match:	54.24%	Indels:	1					
DB:	8	Gaps:	1					
US-09-786-715-2 (1-122) x BTF004710 (1-360)								
QY	2	AlaGluglGlgGlnValIleAlaGcshIsLysIleAspGluTpglGlnGlnLeuGly 21						
Db	7	GCACAAGAGGGGTCAAGTATGTTGGTTCACACGACAGCATGTATGACTGTGCACACTGAT 66						
QY	22	LysTrpIlyAspSergLysLeuValValAspPheThrAlaSerTrpCysGlyPro 41						
Db	67	AAAGCCAAAGATCCACAAACGCTGATGTGATGATTCACTGCTCATGCTGCACCA 126						
QY	42	CysArgAlaIleIleProTyrPheThrGlnLeuAlaLysAsnProAsnValAla 60						
Db	127	TGCGCGATGATGTGTCCAATTTTACAGATTTGGCCAAAGATTCATGTCAGTGCATC 186						
QY	61	PheLeuValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80						
Db	187	TTCTTCAAGTCGATGTTGATGATGACATTCACAGCTTGTCTAAAGAGTTGGTGTGAGGCA 246						
QY	81	MetProThrPheValPheLeuLysGlyLysIleLeuGlnLysSerGlyThrProAla 100						
Db	247	ATGCCAACCTTTGGTTCATTAAGCCGCGCAAGTGTGATGATGCTGCTGTTGCGCAAT 306						
QY	101	LysValGlyLeuSerLysIleLeuGlnLysSerGlyThrProAla 117						
Db	307	AAAGAGATCTTCAGCGCAAAATAGTGAAGCATCTGCTGTTACAACTGCG 357						
RESULT 14								
AK118542		556 bp	mRNA	linear	PLN 06-DEC-2002			
DEFINITION	Arabidopsis thaliana Atlg19730 mRNA for putative thioredoxin,							
LOCUS	complete cds, clone: RAFLI9-77-A10.							
ACCESSION	AK118542							
VERSION	AK118542.1							
KEYWORDS	FLI CDNA; CAP trapper.							
SOURCE	Arabidopsis thaliana (thale cress)							
ORGANISM	Arabidopsis thaliana							
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsis.							
AUTHORS	1 Seki,M., Iida,K., Satou,M., Sakurai,T., Akiyama,K., Ishida,J., Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinzaki,K.							
TITLE	Arabidopsis thaliana full-length cDNA							
JOURNAL	Published only in Database (2002)							
REFERENCE	2 (bases 1 to 556)							
AUTHORS	Seki,M., Iida,K., Satou,M., Sakurai,T., Akiyama,K., Ishida,J., Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinzaki,K.							
TITLE	Direct Submission							
JOURNAL	Submitted (25-NOV-2002) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa							

COMMENT			
<p>230-0045, Japan (E-mail:mekidagc.riken.go.jp, URL: http://pfjweb.gsc.riken.go.jp, Tel:01-45-503-9625, Fax:81-45-503-9366)</p> <p>An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda phage vector (carrienci et al. (2001) Genomics 77:79-90) digested with BamHI and SalI. This clone is in a modified pluscript vector. Please visit our web site (http://pfjweb.gsc.riken.go.jp/) for further details.</p>			
FEATURES			
source	location/Qualifiers		
gene	1..556		
CDs	<p>/organism="Arabidopsis thaliana"</p> <p>/mol_type="mRNA"</p> <p>/culivar="Columbia"</p> <p>/db_xref="taxon:3702"</p> <p>/chromosome="1"</p> <p>/clone="RAFL19-77-A10"</p> <p>/note="common name: thale cress"</p> <p>1..556</p> <p>/gene="At1g19730/F14P1_32"</p> <p>23..382</p> <p>/gene="At1g19730/F14P1_32"</p> <p>/codon_start=1</p> <p>/product="putative thioredoxin"</p> <p>/protein_id="BAC3145.1"</p> <p>/db_xref="gi:26452111"</p> <p>/translation="MAAEEGVICGHFNDVYTVOLDKAKESNKLIVIDFTSMCPPE MIAIPFNDLAKKEMSSAIFFEVDVDELQSVAKKEGVEMPFVFIKGEVYDKLVGNAN KEDIQATVKHTGYVTA"</p>		
BASE COUNT	169 a 88 c 132 g 167 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	7.9e-31	length:	556
Score:	345.50	Matches:	68
Best Local Similarity:	73.50%	Conservative:	18
Query Match:	58.12%	Mismatches:	30
	54.24%	Indels:	1
DB:	8	Gaps:	1
US-09-786-715-2 (1-122) x AK118542 (1-556)			
QY	2	AlaGluglGlyGlnValIleAlaCysHisLysIleAspGluTrpGluGlyGlnLeuGly	21
Db	29	GCACAGAGGGGTCAAGGATGTGGTGTGCACAGCAAGCATGTATGAGACTGTCACTGAT	88
QY	22	LysTrpLysAspSerGluLysLeuValValAspPheThrAlaSerTrpCysGlyPro	41
Db	89	AAACCCAAAGAGATCCACCAACGCTGATTTGTGATTCATTCCTGCTTCATGGTGTCACCA	148
QY	42	CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAla---	60
Db	149	TGCCGCATGATGGTCTCCCAATTTTCAACGATTTGGCCAGGAAGTTCAGTCAAGTCCATC	208
QY	61	PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla	80
Db	209	TTCTTCAAGAGGTGATGTGATGACCTTCAGAGTGTGCTTAAGAAGTTTGGTGTGGAGCA	268
QY	81	MetProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyValAsp	100
Db	269	ATGCGCAACCTTTGTGTTTCATTAAGCCGCGAAGATTTGGTGAATGCTGTGGTGGCAAT	328
QY	101	LysValGlyLeuSerLysLysIleLeuGluLeuSerGlyThrTrpProAla	117
Db	329	AAAGCAAGATCTTCAGCGCAAAATVAGTGAAGCATCTGGTGTAAACAATCGC	379
RESULT 15			
LOCUS	AF051206	641 bp	mRNA linear PLN 18-AUG-1998
DEFINITION	Picea canadensis probable thioredoxin H (SD09) mRNA, complete cds.		
ACCESSION	AF051206		

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 17:46:53 ; Search time 171.507 Seconds

(without alignments)
1920.219 Million cell updates/sec

Title: US-09-786-715-2

Perfect score: 637

Sequence: 1 MAEEGQVIACHKIDEMEGQL.....GLSKITELSGTTAATSTVA 122

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
	Ygapop 10.0	Ygapext 0.5
	Fgapop 6.0	Fgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-o=/cgn2.1/USPTO_pool/US09786715/runat_11082003_150513_6025/app_query.fasta_1.1052
-DB=N_Geneseq_19Jun03 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi
-LIST=45 -DOCALLGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptio -NORR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09786715.ecgn.1.1.874@runat_11082003_150513_6025 -NCPD=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_19Jun03:*

1:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25:	/SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	637	100.0	870	21	AAZ51737	Momordica charantia
2	377.5	59.3	509	22	AAH87768	Peppermint plant o
3	377	59.2	3888	24	ABSS3097	DNA encoding Thlor
4	377	59.2	3888	24	ABN89581	Phaseolin promoter
5	376.5	59.1	470	21	AAC37781	Arabidopsis thalia
6	376	59.0	345	24	AB212358	Arabidopsis thalia
7	376	59.0	345	24	ABN89587	Arabidopsis thalia
8	376	59.0	561	21	AAC51522	Arabidopsis thalia
9	376	59.0	563	21	AAC34121	Arabidopsis thalia
10	376	59.0	3129	24	ABSS3095	DNA encoding thlor
11	376	59.0	3129	24	ABN89579	Phaseolin promoter
12	376	59.0	3888	24	ABSS3096	DNA encoding Oleos
13	376	59.0	3888	24	ABN89580	Phaseolin promoter
14	375	58.9	4935	24	ABN89586	Promoter-Oleoin t
15	375	57.5	738	21	AAZ51739	Glycine max thior
16	361	56.7	574	21	AAZ51738	Catalpa speciosa t
17	360.5	56.6	402	25	ABX21664	Human GDP-mannose
18	357	56.0	328	21	AAA31097	Plant microsateili
19	354	55.6	392	25	ABX18045	Human GDP-mannose
20	354	55.6	601	21	AAZ51740	Glycine max thior
21	352	55.3	346	21	AAA31096	Plant microsateili
22	350	54.9	614	21	AAZ51741	Vernonia mespilifo
23	348	54.6	320	21	AAA31785	Plant microsateili
24	346.5	54.4	590	21	AAC38792	Arabidopsis thalia
25	345.5	54.2	360	24	AB212359	Arabidopsis thalia
26	343	53.8	390	25	ABX19403	Human GDP-mannose
27	343	53.8	686	15	AAQ78205	Gene coding for pr
28	343	53.8	687	21	AAC66375	Rice thiodoxin h
29	337	52.9	560	21	AAQ41961	Arabidopsis thalia
30	335.5	52.7	653	16	AAQ99783	Plant SAR gene pl.
31	335.5	52.7	653	20	AAV62799	Tobacco SAR CHX in
32	335.5	52.7	653	20	AAV81683	Tobacco protein-sy
33	335.5	52.7	653	20	AAV81683	Plant microsateili
34	324.5	50.9	524	21	AAA31942	Arabidopsis thalia
35	324	50.9	292	21	AAC33829	Arabidopsis thalia
36	323	50.7	357	24	AAZ13931	Arabidopsis thalia
37	323	50.7	480	21	AAC36542	Arabidopsis thalia
38	323	50.7	563	21	AAC34211	Arabidopsis thalia
39	323	50.7	562	21	AAC48656	Arabidopsis thalia
40	315	49.5	572	21	AAC52069	Arabidopsis thalia
41	315	49.5	576	25	ABX56868	Arabidopsis thalia
42	314	49.3	353	21	AAA31118	Plant microsateili
43	312	48.8	328	21	AAA31222	Plant microsateili
44	311	48.8	274	21	AAA31859	Plant microsateili
45	310	48.7	356	21	AAA31804	Plant microsateili

ALIGNMENTS

RESULT 1
AAZ51737
ID AAZ51737 standard; CDNA: 870 BP.
AAZ51737;
04-JUL-2000 (first entry)
Momordica charantia thiodoxin cDNA.
Momordica charantia thiodoxin: clone fds.pk0001.e9: chimeric gene;
transgenic plant; seed storage protein; allergenicity; ss.
Momordica charantia.
Key Location/Qualifiers
CDS 49..417

```

FT      /*tag= a
FT      /product= "thioredoxin"
PN      WO200014239-A2.
PD      16-MAR-2000.
XX      07-SEP-1999; 99WO-US20420.
XX      08-SEP-1998; 98US-0099501.
XX      (DUPO ) DU FONT DE NEMOURS & CO E I.
XX      Allen SM, Thorpe CJ, Lu AL;
XX      WPI; 2000-256987/22.
XX      P-PSDB; AAY70479.
DR      New isolated polynucleotide encoding thioredoxin polypeptide is useful
PT      for producing transgenic plants with an altered level of thioredoxin -
XX
XX      Claim 3; Page 28; 33pp; English.
XX
XX      The present cDNA sequence encodes Momordica charantia thioredoxin
CC      protein. The cDNA was derived from clone fds-PK0001.e9, which was
CC      isolated from a cDNA library prepared from M. charantia developing seed
CC      tissue. Chimeric genes encoding all or a portion of the thioredoxin
CC      protein, in sense or antisense orientation are constructed, wherein
CC      expression of the chimeric gene results in production of altered levels
CC      of the thioredoxin protein in a transformed host cell. Thioredoxin is
CC      involved in the disassembly of seed storage proteins during germination
CC      by reducing S-S bonds and in the bread making process. Over expression of
CC      thioredoxin in cereals may reduce the allergenicity of any transgenic
CC      protein engineered into cereal crops with high sulfhydryl content.
XX
XX      Sequence 870 BP; 236 A; 135 C; 209 G; 290 T; 0 other:

```

```

Alignment Scores:
Pred. No.: 5.9e-76 Length: 870
Score: 637.00 Matches: 122
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

```

US-09-786-715-2 (1-122) x AA251737 (1-870)

```

OY      1 MetAlaGluGluGluGluValIleAlaCysHisLysIleAspGluTrpGluGluGluLeu 20
DB      49 ATGGCTGACAGAGGCGAAGTGGTGGTGCATTAAGTAAATGGAGGCAATTA 108
OY      21 GlyLysTrpLysAspSerGluLysLeuValValAspPheThrAlaSerTrpCysGly 40
DB      109 GGAATAATGGAAAGATCTGAGAACTGGTGTGGATTTTACTGCTTCTGCTGGCGG 168
OY      41 ProCysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAla 60
DB      169 CCATGGCCGGGCAATTCCTCATTTTCACAGAAATGGCTTAAGATAACCAATGTCGCT 228
OY      61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
DB      229 TTCTCAAAAGTCACGCTGACGAAATGAACAGTGTGCTAAGCAAGTGGGATTAATGCA 288
OY      81 MetProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAsp 100
DB      289 ATGCCAAGCTTTTTCCTCGAATAAAAGGAAATAATATGAGAAAGATCGTGTGCTGAT 348
OY      101 LysValGlyLeuSerLysLysIleLeuGluLeuSerGlyThrThrProAlaIleThrSer 120
DB      349 AAGTGGGCTGTCGAAGAAATATTAAGAGCTTAAGGAACTACTCCGCTGCTACTTCT 408
OY      121 ThrAla 122
DB      111111

```

```

DB      409 ACTGCT 414
RESULT 2
AAH87768
ID      AAH87768 standard; cDNA; 509 BP.
XX
XX      AAH87768;
AC      25-SEP-2001 (first entry)
DT
XX
DE      Peppermint plant oil gland expressed cDNA 124.
XX
XX      Peppermint; plant oil gland cell; terpenoid essential oil; resin;
XX      genetic mapping; antisense suppression; recombinant expression; ss.
OS      Mentha x piperita.
XX
XX      WO200153319-A1.
PN
XX      26-JUL-2001.
PD
XX
XX      19-JAN-2001; 2001WO-US02567.
PF
XX
XX      20-JAN-2000; 2000US-0177264.
PR
XX      (CROT/) CROTEAU R B.
XX      (LANG/) LANGE B M.
XX      (WILD/) WILDUNG M R.
PI
XX      Croteau RB, Lange BM, Wildung MR;
XX      WPI; 2001-488706/53.
DR
XX
XX      New nucleic acid molecules corresponding to mRNA molecules expressed in
PT      peppermint oil glands for enhancing expression of plant oil gland cell
PT      proteins -
XX
XX      Claim 1; Page 125; 251pp; English.
XX
XX      The invention relates to nucleic acid molecules (AAH87645-AAH88116) that
CC      correspond to all or part of a mRNA molecule expressed in plant oil
CC      gland cells, especially peppermint and plant oil glands that produce
CC      terpenoid essential oils and resins. The nucleic acids are useful for
CC      genetically mapping a plant genome for genes expressed in plant oil
CC      gland cells and to suppress (for example by antisense suppression) or
CC      enhance their expression (for example by genetically transforming a
CC      plant cell with a replicable expression vector that expresses one or more
CC      proteins naturally expressed in plant oil gland cells). The nucleic acids
CC      are also useful for recombinant expression of plant oil gland proteins
CC      required for terpenoid essential oil and/or resin production in bacterial
CC      and/or yeast cells.
XX
XX      Sequence 509 BP; 144 A; 103 C; 129 G; 133 T; 0 other:

```

```

Alignment Scores:
Pred. No.: 2.71e-41 Length: 509
Score: 377.50 Matches: 77
Percent Similarity: 73.33% Conservative: 11
Best Local Similarity: 64.17% Mismatches: 28
Query Match: 59.26% Indels: 4
DB: 22 Gaps: 1

```

US-09-786-715-2 (1-122) x AAH87768 (1-509)

```

OY      4 GluGlyGluValIleAlaCysHisLysIleAspGluTrpGluGluGluLysTrp 23
DB      50 GAAGGACAGGTGATCGGCTGCCACACCTGATTAACGAGACGAGCCTCAAGAAGCGG 109
OY      24 LysAspSerGluLysLeuValValAspPheThrAlaSerTrpCysGlyProCysArg 43
DB      110 AATGATACACAGAAAGTGGTGAAGTGTGATTTTACTGCTTCCGCTGCGGCTTGTGCG 169
OY      44 AlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAlaPheLeuLys 63

```

```
DB 170 TTCATCGCCCTTTTTCGACAAATTTGGCCAAAGAGTTCCCAATGATGACATTTCTCAAG 229
QY 64 ValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAlaMetProThr 83
DB 220 GTGATGTCGATGAGTCAAGTCGCTCTAGTCACTGGCGCAGTCGAGCAATGCCAACCC 289
QY 84 PheValPheLeuLysGlyLysIleIleGluLysIleVal-GlyAlaAspLysValGI 103
DB 290 TTCATCTTCTCCAAAGAGGAAAGATCTTGACACAGTCGTAGGAGGACGACAGAAAGAGA 349
QY 103 yLeuSerLysLysIleLeuGluLeuSerGlyThrThrProAlaAlaThrSerThrAla 122
DB 350 GCTGACGCAATATATGCTAAGCACCCTCAACACA-----GCTACTAGTACTGCT 398

RESULT 3
ABS53097
ID ABS53097 standard; DNA; 3888 BP.
XX
AC ABS53097;
XX
DT 29-NOV-2002 (first entry)
XX
DE DNA encoding Thioredoxin-oleosin fusion protein.
XX
KM Thioredoxin; thioredoxin reductase; gene expression; oleosin;
XX oil body; oleosin-thioredoxin fusion protein; gene; ds.
XX
OS Arabidopsis thaliana.
OS Brassica napus.
OS Synthetic.
XX
FH key Location/Qualifiers
FT CDS 1535..2658
FT /tag= a
FT /product= "Thioredoxin-oleosin fusion protein"
FT exon 1555..2250
FT /tag= b
FT /number= 1
FT intron 2251..2489
FT /tag= c
FT /number= 1
FT exon 2490..2658
FT /tag= d
FT /number= 2
XX
XX US2002088025-A1.
XX
XX 04-JUL-2002.
XX
XX 03-JUL-2001; 2001US-0897425.
XX
XX 22-FEB-1991; 91US-0659835.
XX 16-NOV-1993; 93US-0142418.
XX 30-DEC-1994; 94US-0366783.
XX 25-APR-1997; 97US-0846021.
XX 18-DEC-1998; 98US-0210843.
XX
XX (MOL/ ) MOLONEY M M.
XX PA (DALM/ ) DALMIA B K.
XX
XX Moloney MM, Dalma BK;
XX
XX WPI; 2002-635723/68.
XX
XX Expressing protein, by introducing chimeric nucleotide regulatory
XX PT sequence, sequence encoding fusion protein, having sequence encoding
XX PT protein, oleosin gene and sequence encoding termination region and
XX PT producing protein
XX
XX Example 21, Fig 14; 69pp; English.
XX
XX The invention describes a method of expressing thioredoxin or thioredoxin
```

```
CC reductase (I) in the oil body of a host cell using an oil body protein
CC gene. The method involves introducing a chimeric nucleic acid comprising
CC a first sequence to regulate transcription, a second DNA sequence
CC encoding a fusion polypeptide, comprising a sequence encoding an oleosin
CC gene and sequence encoding (I) and a third sequence encoding a
CC termination region functional in the host cell and growing the host cell
CC to produce a fusion polypeptide. The method or (I) is useful for
CC expression of a thioredoxin or thioredoxin reductase by a host cell. This
CC sequence encodes a oleosin oil body protein fused to Arabidopsis thaliana
CC thioredoxin gene controlled by a phaseolin promoter and phaseolin
CC terminator sequence.
XX
XX Sequence 3888 BP; 1254 A; 722 C; 613 G; 1299 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 5,84e-40 Length: 3888
XX Score: 377.00 Matches: 73
XX Percent Similarity: 71.67% Conservative: 13
XX Best Local Similarity: 60.83% Mismatches: 34
XX Query Match: 59.18% Indels: 0
XX DB: 24 Gaps: 0
XX
XX US-09-786-715-2 (1-122) x ABS53097 (1-3888)
QY 2 AlaGluGluGlyGlnValIleAlaCysHisLysIleAspGluTrpGluGluGlnLeuGly 21
DB 1561 TCGAAGAGAGGACAAAGTGTGCTGCCACACCGGTGACACTGAGACGACGACTTCAG 1620
QY 22 LysTrpLysAspSerGluLysLeuValValAlaAspPheThrAlaSerTrpCysGlyPro 41
DB 1621 AAGGCTAATGATTCACAAACCTTGTGGTGTGATTTCACGCGCTTGTGGTGACCA 1680
QY 42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnProAsnValAlaPhe 61
DB 1681 TGTCTTCATGCTGCCTCATTTCTTCTGCTGATTAACAACTTCATACCTGCTTTTC 1740
QY 62 LeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAlaMet 81
DB 1741 CTCAGAGTTGATACGATGATCAATTTGAAGTCGTGCCAAGTGATGGCCATACAGCGGAG 1800
QY 82 ProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAspLys 101
DB 1801 CCACCTTCATGTTTGTGAAGAGGAGATTTGACAAAGTTGTTGGACCAAGAA 1860
QY 102 ValGlyLeuSerLysLysIleLeuGluLeuSerGlyThrThrProAlaAlaThrSerThr 121
DB 1861 GATGAGCTTCAGTCTACCATTTGCCAAACACTTGCTTAGGCGGATACACGTAAGAGAAC 1920

RESULT 4
ABN89581
ID ABN89581 standard; DNA; 3888 BP.
XX
XX AC ABN89581;
XX
XX 06-SEP-2002 (first entry)
XX
XX Phaseolin promoter-Trxh oleosin-phaseolin terminator DNA SEQ-19.
XX
XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
XX KM oil body; ophthalmological; antidiabetic; cytosolic; antipsoriatic;
XX KM vasotropic; vulnary; antibacterial; immunosuppressive; antitumor;
XX KM food product; milk; wheat; oxidative stress; cataract; diabetes;
XX KM chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
XX KM bronchopulmonary disease; malignancy; reperfusion injury; wound healing;
XX KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
XX KM gastro oesophageal reflux disease; gene; ds.
XX
XX Arabidopsis sp.
XX OS Phaseolus vulgaris.
XX
XX WO200250289-A1.
XX
XX 27-JUN-2002.
```


PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.

PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151302.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159337.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160747.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161406.
PR 25-OCT-1999; 99US-0161405.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 28-OCT-1999; 99US-0162142.

Alignment Scores:
Pred. No.: 3.3e-41
Score: 376.50
Percent Similarity: 73.33%
Best Local Similarity: 60.83%
Query Match: 59.11%
DB: 21
Length: 470
Matches: 73
Conservative: 15
Mismatch: 25
Indels: 7
Gaps: 1

US-09-786-715-2 (1-122) x AAC37781 (1-470)
OY 2 AlagluGluglInVallelAlacyshtlslyslleaspglUtrpglUglInlencly 21

Db 101 TCGAAGAAAGACGATCGCTGCCACACCGTTGACATGGAACGACGCTTCAG 160
QY 22 LysTrpLysAspSerGluLysLeuValValAlaAspPheThrAlaSerTrpCysGlyPro 41
Db 161 AAGGCTAATGAAATCCAAACTCTTGCTGCTGATTCACGGCTTCTTGCTGACCA 220
QY 42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAlaPhe 61
Db 221 TGTGCTTCATGCTCCATCTTCTTGCTGATTTGGCTAAGAACTTCTTAACGTCCTTTC 280
QY 62 LeuLysValAlaAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAlaMet 81
Db 281 CTCGAAGCTTGAATCTGATGAATGAATGAATGCGTGAAGTATGGCGGATACAGCGCATG 340
QY 82 ProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValAlaAspLys 101
Db 341 CCACCTTCATGTTTGGAAAGGAAGGAAAGATTTTGGACAAAGTTGTTGGACCAAGAAA 400
QY 102 ValGlyLeuSerLys-----LysIleLeuGluLeuSerGlyThr 114
Db 401 GATGACCTTCAGTCTACCATTTGCCAAACACTTGCCTGCTCTATTTACACAGTTTGAAGAAC 460
RESULT 6
AB212358
ID AB212358 standard; DNA: 345 BP.
XX
AC AB212358;
XX
DT 21-JUN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 163.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001: 2001MO-US26685.
XX
PR 24-AUG-2000: 2000US-227866P.
XX
PR 26-JUN-2001: 2001US-264647P.
XX
PR 22-JUN-2001: 2001US-300111P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Harper JF, Kreps J, Wang X, Zhu T;
XX
DR WPI: 2002-304127/34.
XX
PT Identifying a stress condition to which a plant cell has been exposed
PT and producing plants with increased tolerance to these abiotic stresses
PT
XX
PS Claim 144; SEQ ID NO 163; 577pp + Sequence Listing; English.
XX
PS
XX
CC The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising:
CC (a) contacting nucleic acid representative of expressed polynucleotides
CC in the plant cell with an array or probes representative of the plant
CC cell genome; and
CC (b) detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by

CC the European Patent Office.
XX
SQ Sequence 345 BP; 90 A; 68 C; 90 G; 97 T; 0 other;
Alignment Scores:
Pred. No.: 2,47e-41 Length: 345
Score: 376.00 Matches: 71
Percent Similarity: 77.57% Conservative: 12
Best Local Similarity: 66.36% Mismatches: 24
Query Match: 59.03% Indels: 0
DB: 24 Gaps: 0
US-09-786-715-2 (1-122) x AB212358 (1-345)
QY 2 AlagluGluLysIleValIleAlaCysHisLysIleAspGluTrpGluGluIleGly 21
Db 7 TCGAAGAAAGACGATCGCTGCCACACCGTTGACATGGAACGACGCTTCAG 66
QY 22 LysTrpLysAspSerGluLysLeuValValAlaAspPheThrAlaSerTrpCysGlyPro 41
Db 67 AAGGCTAATGAAATCCAAACTCTTGCTGCTGATTCACGGCTTCTTGCTGACCA 126
QY 42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAlaPhe 61
Db 127 TGTGCTTCATGCTCCATCTTCTTGCTGATTTGGCTAAGAACTTCTTAACGTCCTTTC 186
QY 62 LeuLysValAlaAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAlaMet 81
Db 187 CTCGAAGCTTGAATCTGATGAATGAATGCGTGAAGTATGGCGGATACAGCGCATG 246
QY 82 ProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValAlaAspLys 101
Db 247 CCACCTTCATGTTTGGAAAGGAAGGAAAGATTTTGGACAAAGTTGTTGGACCAAGAAA 306
QY 102 ValGlyLeuSerLysIle 108
Db 307 GATGACCTTCAGTCTACCATTT 327
RESULT 7
ABN89587
ID ABN89587 standard; DNA: 345 BP.
XX
AC ABN89587;
XX
DT 06-SEP-2002 (first entry)
XX
DE Arabidopsis thaliana thioedoxin h (Trx h 1) DNA SEQ ID NO:38.
XX
KW Multimeric protein; redox protein; thioedoxin; thioedoxin reductase;
KW oil body; ophthalmological; antidiabetic; cytoskeletal; antiproliferic;
KW vasotropic; vulnereary; antibacterial; immunosuppressive; antitumor;
KW food product; milk; wheat; oxidative stress; cataract; diabetes;
KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
KW gastro intestinal; bleeding; intestinal; bowel disease; ulcer;
KW gastro oesophageal reflux disease; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200250289-A1.
XX
PD 27-JUN-2002.
XX
PF 19-DEC-2001: 2001MO-US50240.
XX
PR 19-DEC-2000: 2000US-0742900.
XX
PR 05-JUL-2001: 2001US-302885P.
XX
PR 04-DEC-2001: 2001US-0006038.
XX
PA (SEMB-) SEMBIOSYS GENETICS INC.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Van Rooijen G, Deckers H, Helfeltz PB, Briggs SP, Dalmia BK;

PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140655.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143644.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 09-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 10-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.

PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:

Pred. No.:	4,96e-41	Length:	561
Score:	376.00	Matches:	71
Percent Similarity:	77.57%	Conservative:	12
Best Local Similarity:	66.36%	Mismatches:	24
Query Match:	59.03%	Indels:	0
DB:	21	Gaps:	0

US-09-786-715-2 (1-122) x AAC51522 (1-561)

OY 2 AAlaGlUGlUGlValIleAlaCySHISLysIleAspIuTrpGlUGlUGlInLeUGly 21
Db 100 TCGAGAGAAAGCAAGATCGCTGCCACACCGTTGACATGGAAGCAAGCAAGCTTCAG 159
OY 22 LysTrpLysAspSerGluLysLeuValValAspPheThrLAserTrpCysGlyPro 41
Db 160 AAGGCTAATGAATCAAAACCTGTGTGCTGGATTTCAGGCTCTTGTGTGGACCA 219
OY 42 CysArgAlaIleLeaProTyRpheThrGluLeuAlaLysAsnAsnProAsnValAlaPhe 61
Db 220 TGTGCTTTCATCGCTCATCTTGTGCGATTGTGCTAAGAAACTTCTAAGCGTCTTTC 279

[illegible]

```

PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-015659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:

4.99e-41
376.00
77.378

Length: 563
Matches: 71
Conservative: 12

```

Best Local Similarity: 66.36% Mismatches: 24
Query Match: 59.03% Indels: 0
DB: 21 Gaps: 0
US-09-786-715-2 (1-122) x AAC34121 (1-563)

QY 2 AlaGluGluGlyGlnValIleAlaCysHisLysIleAspGluTrpGluGlyGlnLeuGly 21
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 102 TCGAAGACAGACAAAGATCGCGCCACACCGTGAAGATGACAGACAGACACTTCAG 161
   TCGAAGACAGACAAAGATCGCGCCACACCGTGAAGATGACAGACAGACACTTCAG 161

QY 22 LysTrpLysAspSerGlyLysLeuValValValAspPheThrAlaSerTrpCysGlyPro 41
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 162 AAGCCTAATGATCAAACTCTTGCGTGAATTCACGCGCTCTTGCGTGAATTC 221
   AAGCCTAATGATCAAACTCTTGCGTGAATTCACGCGCTCTTGCGTGAATTC 221

QY 42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAlaPhe 61
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 222 TGTCGTTTCATCGCTCATCTTTCGATTCGATTCGTAAGAAACTCCTAACGTCCTTTC 281
   TGTCGTTTCATCGCTCATCTTTCGATTCGATTCGTAAGAAACTCCTAACGTCCTTTC 281

QY 62 LeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAlaMet 81
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 282 CTCAGAGCTGATACGATGATGAATGAAGTCGCGCAAGTGAATGCGCATACAGCGATG 341
   CTCAGAGCTGATACGATGATGAATGAAGTCGCGCAAGTGAATGCGCATACAGCGATG 341

QY 82 ProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAspLys 101
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 342 CCACCTTCATGTTTGAAGAGGAGGAAATTTGACAAAGTTGTGGAGCCAGAGAA 401
   CCACCTTCATGTTTGAAGAGGAGGAAATTTGACAAAGTTGTGGAGCCAGAGAA 401

QY 102 ValGlyLeuSerLysIle 108
   ::::::::::::::
Db 402 GATGAGCTTCAGTCTACATT 422
   GATGAGCTTCAGTCTACATT 422

RESULT 10
ABBS3095
ID ABBS3095 standard; DNA; 3129 BP.
XX
AC ABBS3095;
XX
DT 29-NOV-2002 (first entry)
XX
XX DNA encoding thioredoxin-phaseolin fusion protein.
XX
DE Thioredoxin; thioredoxin reductase; gene expression; oleosin;
XX
KW oil body; gene; ds; thioredoxin reductase; phaseolin.
XX
XX Arabidopsis thaliana.
XX
OS Phaseolus vulgaris.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1555..1899
   /*tag= a
   /product= "thioredoxin-phaseolin fusion protein"

US2002088025-A1.
XX
PD 04-JUL-2002.
XX
PF 03-JUL-2001; 2001US-0897425.
XX
PR 22-FEB-1991; 91US-0659835.
PR 16-NOV-1993; 93US-0142418.
PR 30-DEC-1994; 94US-0366783.
PR 25-APR-1997; 97US-0846021.
PR 18-DEC-1998; 98US-0210843.
XX
PA (MOLC/) MOLONEY M. M.
PA (DALM/) DALMIA B. K.
XX
PI Moloney MM, Dalmlia BK;
XX
DR WPI: 2002-635723/68.
DR P-PSDB; ABG32916.
XX
PT Expressing protein, by introducing chimeric nucleotide regulatory

```

PT sequence, sequence encoding fusion protein, having sequence encoding
PT protein, oleosin gene and sequence encoding termination region and
producing protein

XX Example 21; Fig 12; 69pp; English.

XX The invention describes a method of expressing thioredoxin or thioredoxin
CC reductase (I) in the oil body of a host cell using an oil body protein
CC gene. The method involves introducing a chimeric nucleic acid comprising
CC a first sequence to regulate transcription, a second DNA sequence
CC encoding a fusion polypeptide, comprising a sequence encoding an oleosin
CC gene and sequence encoding (I) and a third sequence encoding a
CC termination region functional in the host cell and growing the host cell
CC to produce a fusion polypeptide. The method or (I) is useful for
CC expression of a thioredoxin or thioredoxin reductase by a host cell. This
CC sequence represents an Arabidopsis thaliana thioredoxin gene controlled
CC by a phaseolin promoter and terminator for use in an expression vector.

XX Sequence 3129 BP; 1051 A; 549 C; 439 G; 1090 T; 0 other;

Alignment Scores:

Pred. No.:	5,84e-40	Length:	3129
Score:	376.00	Matches:	71
Percent Similarity:	77.57%	Conservative:	12
Best Local Similarity:	66.36%	Mismatches:	24
Query Match:	59.03%	Indels:	0
DB:	24	Gaps:	0

US-09-786-715-2 (1-122) x ABS53095 (1-3129)

QY 2 AAGAGUGUGIYGVINVAIIIEALACYSHTLSYLSLEASPGIUTRPLUGLGNLEUGLY 21

DB 1561 TCGGAAGAGACGACAACTGATCGCTGCCACACCGTTGACACATGACAGCAGCCTTCAG 1620

QY 22 LYSTPLYSASPSEICLULYSLEUVALVALASPPHERHVALASERTPCYSGLYPRO 41

DB 1621 AAGGCTAATGAACTCCAAACTCTGTGGTGATTGATTCACGGCTCTTGTTGGTGGACCA 1680

QY 42 CYSATGALAILLEALAPROTYPHERHGLULEUALALYSASNAASNPRAASNAVALALAPHE 61

DB 1681 TGTGCTTCATCGCTCCATCTGTTGCTGATTTGGCTAAAGAACTTCCTAACGCTTTTC 1740

QY 62 LEULYSVALASPVVALASPLULEUASNSERVALALASERTYRPLUGLGNLEASNAIAME 81

DB 1741 CTCAGAGTGTACATCATTAATTTGAAGTGGCGCAAGATTTGGCGCATACAGGCGATG 1800

QY 82 PROTHPHEVALPHELEULYSLSYGLYSLEILEGLULYSLEVALGLYALASPLYS 101

DB 1801 CCAACCTTCATGTTTGAAGAGAGGAGATTTCGACAAAGTTGTTGGAGCCAGAGAA 1860

QY 102 VALGLYLEUSERLSYSTLE 108

DB 1861 GATGAGCTTCAGCTACCAATT 1881

DB ABN89579

ID ABN89579 standard; DNA; 3129 BP.

AC ABN89579;

DT 06-SEP-2002 (first entry)

DE Phaseolin promoter-Arabidopsis Trxh-phaseolin terminator DNA SEQ.14.

XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
KM oil body; ophthalmological; antidiabetic; cytosolic; antipsoriatic;
KM vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
KM food product; milk; wheat; oxidative stress; cataract; diabetes;
KM chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
KM gastro intestinal bleeding; intestinal disease; ulcer;
XX gastro oesophageal reflux disease; gene; ds.

OS Arabidopsis sp.
OS Phaseolus vulgaris.

XX WO200250289-A1.

XX 27-JUN-2002.

PF 19-DEC-2001; 2001MO-US50240.

XX 19-DEC-2000; 2000US-0742900.

PR 05-JUL-2001; 2001US-302885P.

PR 04-DEC-2001; 2001US-0006038.

XX (SEMB-) SEMBIOSYS GENETICS INC.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;

PI Del Val G, Zaplachinski S, Moloney M;

XX WPI: 2002-508806/54.

DR P-PSDB; ABP60680.

XX Producing oil body associated with recombinant multimeric protein

PT complex e.g. redox proteins and immunoglobulins comprises producing

PT recombinant polypeptides capable of forming the complex in cells

PT comprising oil bodies -

XX Example 2; Page 165-166; 362pp; English.

XX The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating
CC with P2 to form the MPC and associating the complex with an occlusion
CC body (OB) through an OB-targeting-protein capable of associating with OB
CC and P1. M1 is useful for producing an oil body associated with a
CC recombinant MPC. The oil bodies are further formulated for use in the
CC preparation of a food product such as milk or wheat based food product,
CC personal care product which reduces the oxidative stress on the surface
CC area of the human body or used to lighten the skin, or a pharmaceutical
CC composition used to treat chronic obstructive pulmonary disease (COPD),
CC cataracts, diabetes, emphysema, bronchiopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 and ABP60677
CC to ABP60964 represent sequence given in the exemplification of the
CC present invention.

XX Sequence 3129 BP; 1051 A; 549 C; 439 G; 1090 T; 0 other;

Alignment Scores:

Pred. No.:	5,84e-40	Length:	3129
Score:	376.00	Matches:	71
Percent Similarity:	77.57%	Conservative:	12
Best Local Similarity:	66.36%	Mismatches:	24
Query Match:	59.03%	Indels:	0
DB:	24	Gaps:	0

US-09-786-715-2 (1-122) x ABN89579 (1-3129)

QY 2 AAGAGUGIYGVINVAIIIEALACYSHTLSYLSLEASPGIUTRPLUGLGNLEUGLY 21

DB 1561 TCGGAAGAGACGACAACTGATCGCTGCCACACCGTTGACACATGACAGCAGCCTTCAG 1620

QY 22 LYSTPLYSASPSEICLULYSLEUVALVALASPPHERHVALASERTYRPLUGLGNLEASNAIAME 41

DB 1621 AAGGCTAATGAACTCCAAACTCTGTGGTGATTGATTCACGGCTCTTGTTGGTGGACCA 1680

QY 42 CYSATGALAILLEALAPROTYPHERHGLULEUALALYSASNAASNPRAASNAVALALAPHE 61

DB 1681 TGTGCTTCATCGCTCCATCTGTTGCTGATTTGGCTAAAGAACTTCCTAACGCTTTTC 1740

QY 62 LEULYSVALASPVVALASPLULEUASNSERVALALASERTYRPLUGLGNLEASNAIAME 81

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 19:18:57 ; Search time 45.2132 Seconds
(without alignments)
1190.995 Million cell updates/sec

Title: US-09-786-715-2

Perfect score: 637

Sequence: 1 MAERGOVACHRIDEMEQ.....GLSKRIELSGTTPATSTA 122

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Command line parameters:

-MODEL=frame+P2n.model -DEV=xlp
-O=/cgn2.1/USPTO_spool/US09786715/runat_11082003.150515.6083/app.query.fasta_1.1052
-DB-issued=Patents_NA -QEMT=fastap -SUFFIX=rii -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09786715.ecgn.1.1.175-@runat_11082003.150515.6083 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOUTERY -NEG.SCORES=0 -WAIT -DSPELOCK=100 -LONGLOC
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents_NA:*
1: /cgn2.6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2.6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2.6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2.6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2.6/ptodata/1/ina/PCUTS.COMB.seq:*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	335.5	52.7	653	1	US-08-181-271A-103
2	335.5	52.7	653	1	US-08-449-315-103
3	335.5	52.7	653	1	US-08-444-803-103
4	335.5	52.7	653	1	US-08-449-043-103
5	335.5	52.7	653	1	US-08-456-265A-103
6	335.5	52.7	653	1	US-08-455-416-103
7	335.5	52.7	653	1	US-08-455-244-103
8	335.5	52.7	653	1	US-08-454-876-103
9	335.5	52.7	653	2	US-08-457-364-103
10	335.5	52.7	653	2	US-08-456-262-103
11	335.5	52.7	653	2	US-08-456-240-103
12	335.5	52.7	653	2	US-08-455-736-103

13	335.5	52.7	653	2	US-08-971-217-103
14	335.5	52.7	653	3	US-09-350-600-103
15	302	47.4	369	4	US-09-540-014-1
16	298	46.8	382	4	US-09-540-014-3
17	298	46.8	393	4	US-09-540-014-5
18	231	36.3	557	4	US-09-404-879A-88
19	231	36.3	557	4	US-09-338-933-88
20	231	36.3	557	4	US-09-215-681-88
21	231	36.3	581	4	US-09-601-144-67
22	231	36.3	594	4	US-09-404-879A-87
23	231	36.3	594	4	US-09-338-933-87
24	231	36.3	594	4	US-09-215-681-87
25	231	36.3	601	4	US-09-404-879A-133
26	231	36.3	601	4	US-09-338-933-133
27	231	36.3	601	4	US-09-215-681-133
28	231	36.3	624	3	US-09-385-982-526
29	231	36.3	630	3	US-08-180-371-5
30	231	36.3	630	3	PCR-US92-05707-5
31	230	36.1	630	3	US-08-180-371-17
32	223.5	35.1	318	4	US-09-313-294A-5868
33	216	33.9	605	3	US-09-385-982-485
34	210	33.0	631	3	US-09-385-982-174
35	206	32.3	914	1	US-08-386-729A-9
36	189	29.7	278	4	US-09-313-294A-5840
37	178.5	28.0	7096	4	US-09-221-017B-373
38	172.5	27.1	564	2	US-08-775-978-2
39	172	27.0	729	2	US-08-826-910-2
40	171.5	26.9	336	4	US-09-134-001C-1022
41	170	26.7	4403765	3	US-09-103-840A-2
42	170	26.7	4411529	3	US-09-103-840A-1
43	167.5	26.3	1230025	4	US-09-198-452A-1
44	161	25.3	438	4	US-09-328-352-1234
45	152.5	23.9	4969	1	US-08-260-582-76

ALIGNMENTS

RESULT 1
US-08-181-271A-103
; Sequence 103, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesting, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Meyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Sherioka C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

1 SOFTWARE: PatentIn Release #1.0, Version #1.25
2 CURRENT APPLICATION DATA:
3 APPLICATION NUMBER: US/08/181,271A
4 FILING DATE: 13-JAN-94
5 CLASSIFICATION: 435
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US 08/093,301
8 FILING DATE: 16-JUL-1993
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 07/937,197
11 FILING DATE: 6-NOV-1992
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 07/678,378
14 FILING DATE: 1-APR-1991
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 07/305,566
17 FILING DATE: 6-FEB-1989
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 07/165,667
20 FILING DATE: 8-MAR-1988
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 08/042,847
23 FILING DATE: 6-APR-1993
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 07/632,441
26 FILING DATE: 21-DEC-1990
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 07/425,504
29 FILING DATE: 20-OCT 1989
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 07/848,506
32 FILING DATE: 6-MAR-1992
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: US 07/768,122
35 FILING DATE: 27-SEP-1991
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: US 07/580,431
38 FILING DATE: 7-SEP-1990
39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER: US 07/368,672
41 FILING DATE: 20-JUN-1989
42 PRIOR APPLICATION DATA:
43 APPLICATION NUMBER: US 07/329,018
44 FILING DATE: 24-MAR-1989
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: US 08/045,957
47 FILING DATE: 12-APR-1993
48 ATTORNEY/AGENT INFORMATION:
49 NAME: Elmer, James Scott
50 REGISTRATION NUMBER: 36,129
51 REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727
52 TELECOMMUNICATION INFORMATION:
53 TELEPHONE: (919)541-8614
54 TELEFAX: (919)541-8689
55 INFORMATION FOR SEQ ID NO: 103:
56 SEQUENCE CHARACTERISTICS:
57 LENGTH: 653 base pairs
58 TYPE: nucleic acid
59 STRANDEDNESS: single
60 TOPOLOGY: linear
61 MOLECULE TYPE: DNA (genomic)
62 US-08-181-271A-103
63
64 Alignment Scores:
65 Pred. No.: 1,49e-35 Length: 653
66 Score: 335.50 Matches: 65
67 Percent Similarity: 72.13% Conservative: 23
68 Best Local Similarity: 53.28% Mismatches: 30
69 Query Match: 52.67% Indels: 4
70 DB: 1 Gaps: 1
71
72 US-09-786-715-2 (1-122) x US-08-181-271A-103 (1-653)

```

```

Oy      2  Alghnglglgylvnlvalllaecyshsllytjleaspglutrgluclglnleugly 21
Db      72  TCCGAGGAGGGACAAAGTGTTCGGCTGCCACAAGTTGAGGAATGCACGACTACTTAAC 131
Oy      22  LysTrPlyspserserLulYsLeuValValaaSpherhralaserTPCyaglyPro 41
Db      132 AAMGGCGGTGACACTAAGAACAACGCGTGCGATTTTACGTCTCATGTGGGSCCT 191
Oy      42  CysarqAlalleaLProfyrphethrGluleualalyAsnAsnPfoAsNValAlaPhe 61
Db      192 TGCGGTTTTATTGCCCAATTCCTGTGCTGACATTTGCTAAGAGAGATGCCCAATTTATTC 251
Oy      62  LeuLyValaspYalaspGluleuAsnservAlalaSer-LysTrPgLuileasAlaMe 81
Db      252 CTGAGAGTTGATGTTTATGATGACGAAGACTGTTTCAGCGGGAAGGAGACTGTGGAGGCAT 311
Oy      81  tProrhpheValpheLeuLeuLYsGLYsIleellegLulYsIleValglYalaasPLY 100
Db      312 GCCAACCTTTGCTCCTCATTTAAAGATGGAATAAGACTGGACAGAGTTGTGTGCCAAGAA 371
Oy      101 sValglYLeuSerLYsLYsIleleuGluleuSerGLYThrThrPrroAlaalatrserTh 121
Db      372 AGAGAGATTGCACAGACCACCATGATGAGCATGCTCTCT-----CCTGCTACTGTAC 422
Oy      121 rala 122
Db      423 TGCT 426

RESULT 2
US-08-449-315-103
: Sequence 103, Application US/08449315
: Patent No. 5650505
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperrison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,315
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301

```

;; FILING DATE: 16-JUL-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/937,197
;; FILING DATE: 6-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/678,378
;; FILING DATE: 1-APR-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/305,566
;; FILING DATE: 6-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/165,667
;; FILING DATE: 8-MAR-1988
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/042,847
;; FILING DATE: 6-APR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/632,441
;; FILING DATE: 21-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/425,504
;; FILING DATE: 20-OCT-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/848,506
;; FILING DATE: 6-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/768,122
;; FILING DATE: 27-SEP-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/580,431
;; FILING DATE: 7-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/368,672
;; FILING DATE: 20-JUN-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/329,018
;; FILING DATE: 24-MAR-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/045,957
;; FILING DATE: 12-APR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Elmer, James Scott
;; REGISTRATION NUMBER: 36,129
;; REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919)541-8614
;; TELEFAX: (919)541-8689
;; INFORMATION FOR SEQ ID NO: 103:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 653 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-449-315-103

Alignment Scores:
Pred. No.: 1,49e-35 Length: 653
Score: 335.50 Matches: 65
Percent Similarity: 72.13% Conservative: 23
Best Local Similarity: 53.28% Mismatches: 30
Query Match: 52.67% Indels: 4
DB: 1 Gaps: 1

US-09-786-715-2 (1-122) x US-08-449-315-103 (1-653)
QY 2 Aaagluglglglnvalilleaacyshstlyslleaapglutrpgluglgnleugly 21
DB 72 TCCGAGGAGGAGCAGGTGTTCGCGTCCCAAGAGTTGAGATGGAAGAGTACTTCAAG 131
QY 22 lylstrplyaspserglulysleuvalvalvalaaspherhralaserttrpcysglypro 41
DB 132 AAAGCGTTGAGACTAAGAACTGCTGCTGCATTTTACTGCTTCATGCTGCGGSCCT 191

QY 42 CysArgAlaIleAlaIleProTyrPheThrGluLeuAlaIleLysAsnProAsnValAlaIlePhe 61
DB 192 TGCCGTTTATGCCCCCAATTCCTTCTGCTGACATTGTAAGAAAGATGCCCATGTTATATTC 251
QY 62 LeuLysValAspValAspGluLeuAsnSerValAlaIleSer-LysTrpGluIleAsnLle 81
DB 252 CTCAGGTTGATGTTTATGATGACTGAAGACTGTTTCAGCCGGAATGAGTGTGAGGCAT 311
QY 81 tProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValAlaIleAspLys 101
DB 312 GCCAACTTTGCTCTCATTAAGATGGAAGAAAGAGGAGAGAGTGTGTCGCCAAGAA 371
QY 101 sValGlyLeuSerLysLysIleLeuGluLeuSerGlyThrProAlaIleThrSerh 121
DB 372 AGAGGAGTTCAGACAGACCATGATGTAAGCATGCTGCT-----CCTGCTACTGTCTAC 422
QY 121 rAla 122
DB 423 TGCT 426

RESULT 3
US-08-444-803-103
; Sequence 103, Application US/08444803
; Patent No. 5654414
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesling, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,803
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991

FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8367
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-456-265A-103

Alignment Scores:
Pred. No.: 1,49e-35 Length: 653
Score: 335.50 Matches: 65
Percent Similarity: 72.13% Conservative: 23
Best Local Similarity: 53.28% Mismatches: 30
Query Match: 52.67% Indels: 4
DB: 1 Gaps: 1

US-09-786-715-2 (1-122) x US-08-456-265A-103 (1-653)

QY 2 Alagluglugglgnvalilalaqyshtlsytleasplurpuglgnleuclly 21
Db 72 TCCGAGGAGGACAGAGTTCGGCTGCCACAGAGTTGAGAGAGGACGACTTAAAG 131
QY 22 LysTrpLysAspSerGluLysLeuValValAlaSpheThAlaSerTrpCysGlyPro 41
Db 132 AAAGCGCTGAGACTAGAAAGCTGGTGGTGCATTTTACGCTTCATGGTGGGSCCT 191
QY 42 CysArgAlaIleAlaProTrpPheThGlnLeuAlaLysAsnAsnProAsnValAlaPhe 61
Db 192 TGCCGCTTTATTCGCCCAATTCCTGCTGACATTCCTAAGAAGATGCTTATTTTC 251
QY 62 LeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluLeuAlaIle 81
Db 252 CTCAAGGTTATGTTGATGAGACTGAGACTGTTTCACGGGAATGGAGTGGAGCAAT 311
QY 81 tProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAspLys 101
Db 312 GCCAAGCTTTGCTTCATTAAGATGAGAAAGATGACAGAGATGTTGTCGCAAGAA 371
QY 101 sValGlyLeuSerLysLysIleLeuGluLeuSerGlyThThProAlaIleAsnSerTh 121
Db 372 AGAGGAGTTCACACAGACCATTAAGTGAAGATGCTGCT-----CCTGCTACTGTAC 422
QY 121 caIa 122
Db 423 TGCT 426

RESULT 6
US-08-455-416-103
Sequence 103, Application US/08455416
Patent No. 5777200
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian

APPLICANT: Meigs, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Spertson, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993

```
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CCG 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-455-416-103

Alignment Scores:
Pred. No.: 1.49e-35 Length: 653
Score: 335.50 Matches: 65
Percent Similarity: 72.13% Conservative: 23
Best Local Similarity: 53.28% Mismatches: 30
Query Match: 52.67% Indels: 4
DB: 1 Gaps: 1

US-09-786-715-2 (1-122) x US-08-455-416-103 (1-653)
QY 2 ATAGTUGLUGLVLGVLVALLLEALACYSHTLSYLSLEASPGLUTRPLUGLGLNLEUGLY 21
   ::::::::::::::::::::
DB 72 TCCGAGAGGAGGACCAAGTGTTCGCGTCCACAGAGTTGAGAGATGAGACGACTTCAAG 131
   ::::::::::::::::::::
QY 22 LYSTPLYSASPSPERLULYSLEUVALVALJASPPHETRALASERTPCYSGLYPRO 41
   ::::::::::::::::::::
DB 132 AAGCGGTGAGACTAGAGAACTGGTGGTGGATTTCAGTCTCAAGTGGCGSCT 191
   ::::::::::::::::::::
QY 42 CYSATGALAILALAPROTGYRPHETRGULLEUALALYASNSAPROASNYALALAPHE 61
   ::::::::::::::::::::
DB 192 TCCCGTTTATGCCCCAATCTCTGCTGACATGCTAAGAGATGCCCATGTTATATTC 251
   ::::::::::::::::::::
QY 62 LELYSVALASPVALASPLULSUSNSERVALALASER-LYSTPRGLUILASNNLAME 81
   ::::::::::::::::::::
DB 252 CTCAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
   ::::::::::::::::::::
QY 81 TPROTHRPHETVALPHELEULYSLSYLSLEILEGLULYSLEVALGLVALASPLY 101
   ::::::::::::::::::::
DB 312 GCCAAGTTTGTCTTCATTAAGATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 371
   ::::::::::::::::::::
QY 101 sVALGLYLEUSERLYSLYSLEUGLULSUSERGLYTHRPRIOALALATHRSETH 121
   ::::::::::::::::::::
DB 372 AGAGGAGTTGCAGAGACCATAGTGAAGCATGCTGCT-----CCTGCTACTGTGAC 422
   ::::::::::::::::::::
QY 121 rALA 122
   |||
DB 423 TCCT 426

RESULT 7
US-08-455-244-103
Sequence 103, Application US/08455244
Patent No. 5789214
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
```

```
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CCG 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
```

```

? INFORMATION FOR SEQ ID NO: 103:
?   SEQUENCE CHARACTERISTICS:
?       LENGTH: 653 base pairs
?       TYPE: nucleic acid
?       STRANDEDNESS: single
?       TOPOLOGY: linear
?   MOLECULE TYPE: DNA (genomic)
US-08-455-244-103

Alignment Scores:
Pred. No.:      1.49e-35          Length:      653
Score:          335.50           Matches:    65
Percent Similarity: 72.13%      Mismatches: 20
Best Local Similarity: 53.28%   Indels:     3
Query Match:     52.67%         Gaps:       1
DB:              1              1

US-09-786-715-2 (1-122) x US-08-455-244-103 (1-653)
QY      2  ALaGlUGlUGlYgInValIleAlAcYSnISLysIILeAspGIUTRpGluGIgInLeugly 21
        ::::::::::::::::::::| | | | | | | | | | | | | | | | | | | | | |
Db      72  TCCGAGAGGAGCAACAGTGTTCGGCTGCACCACAAGTGTAAGAATGCAACAGACTTCAAG 133
QY      22  LysTRPlyAspSerCIULySLeuValValAlasphethrAlaserTPCySGlyPro 41
        ||| : | | | | | | | | | | | | | | | | | | | | | |
Db      132 AAAGCGGTGAGCTAAGAAACGTGGGTGGTCGATTTCATGCTCATGGTGGGSCT 191
QY      42  CysArgAlaIleAlaProTyRphethrGluLeuAlaLysAsnProsnValAlaPhe 61
        ||||| | | | | | | | | | | | | | | | | | | | | |
Db      192 TGCCGCTTTATTTGCCCAATTCCTGTGACATTCCTAAGAAGATGCCCACTATATATTC 251
QY      62  LeuLySValAspValAspGluLeuSnSerValAlaser-LysTRPGluIleAsnAlame 81
        ||||| | | | | | | | | | | | | | | | | | | | | |
Db      252 CTCGAAGTGTGATGTGATGATCACTGAAGACTGTTTCACGGGAATGAGTGTGGAGCAAT 311
QY      81  tPrOThrPheValPheLeuLySLySGlyLysIleIleGluLySIleValIGlyAlaaply 101
        ||||| | | | | | | | | | | | | | | | | | | | | |
Db      312 GCCAACTTTGTCTTATTTAAAGATGGAAGAAAGACTGGACAGAGTGTGGTCCAAAGAA 371
QY      101 sValIgLyLeuSerLySLySLeuGluLeuSerGIYThrThrProAlaArhSrTh 121
        ||| : | | | | | | | | | | | | | | | | | | | |
Db      372 AGAGGAGTTGCAACAGCACCATAGTAGAGCATGCTGCT-----CCTGCTACTGTCAC 422
QY      121 rAla 122
        ||||
Db      423 TGCT 426

RESULT 8
US-08-454-876-103
? Sequence 103, Application US/08454876
? Patent No. 5804693
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Sherlica C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
NUMBER OF INVENTIONS: DNA SEQUENCES AND USES THEREOF
CORRESPONDENCE ADDRESS: 106

```

ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0. Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/L/CGC 1722
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-454-876-103

Alignment Scores:

Pred. No.:	1.49e-35	Length:	653
Score:	335.50	Matches:	65
Percent Similarity:	72.13%	Conservative:	23
Best Local Similarity:	53.28%	Mismatches:	30
Query Match:	52.67%	Indels:	4
DB:	1	Gaps:	1

US-09-786-715-2 (1-122) x US-08-454-876-103 (1-653)

QY 2 AAlagluglgiygiInvalIleAlaCyshIslyslleapglutprgluglgiInleugly 21
:::|||||:::|||||
DB 72 TCCGAGGAGGAGCAAGTTCGGCTGCCACAGAGTGAGATGAGAGAGTCTTATTC 131
QY 22 LysTrpLysAspSerGluLysLeuValValAlaAspPheTrpCysGlyPro 41
|||:::|||||
DB 132 AAAGCGCTTGAGACTAAAGAACTGGTGGTGTGCTGATTTACTGCTCATGTCGCGSCCT 191
QY 42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAlaPhe 61
|||||:::|||||
DB 192 TCCCGTTTATTTGCCCATTTCTTCTGACATGCTAGAGAGATGCCCATGTTATTC 251
QY 62 LeuLysValaAspValaAspGluLeuAsnSerValAlaSer-LysTrpGluIleAsnAlaMe 81
|||||:::|||||
DB 252 CTCAGAGTTGATGTTGATGAACTGTAAGACTGTTTCAGCGGGAAGTGAAGTGGAGCAAT 311
QY 81 tProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAspLys 101
|||||:::|||||
DB 312 GCCAAGCTTTCTTCATTAAGAGGAAAGAGTGAAGAGAGTGTGGTGGCCAGAA 371
QY 101 sValGlyLeuSerLysLysIleLeuGluLeuSerGlyThrProAlaIleAsnThSerTh 121
|||:::|||||
DB 372 AGAGAGTTGACGACGACCATGATGATGATGCTGCT-----CCTGCTACTGTAC 422
QY 121 rAla 122
|||
DB 423 TGCT 426

RESULT 9

US-08-457-364-103
; Sequence 103, Application US/08457364
; Patent No. 5847258

GENERAL INFORMATION:

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Melms, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESS: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,364
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-457-364-103

Alignment Scores:
Pred. No.: 1.49e-35
Score: 335.50
Percent Similarity: 72.13%
Best Local Similarity: 53.28%

Length: 653
Matches: 65
Conservative: 23
Mismatches: 30

Db 192 TCCCGTTTATTCCTCCCAATTCCTGACATTCCTAAGATGCCCCCATGTTATATTC 251
Qy 62 LeuLVaValAspValAspGluLeuAsnSerValAlaSer-LysTrpGluIleAsnAlaMe 81
Db 252 CTCAGAGTTGATGTGATGAGTGAAGACACTGTTTCACGGGAATGGAGTGTGAGGCAAT 311
Qy 81 tProthPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAspLy 101
Db 312 GCCAAGTTTGTCTTCACTTAAGATGGAAGAAAGATGACAGATGTTGTGCGCAAGAA 371
Qy 101 sValGlyLeuSerLysLysLysIleLeuGluLeuSerGlyThrThrProAlaIleThrSerTh 121
Db 372 AGAGAGTTGACACAGACCATAGTGAAGCATGCTGCT -----CCTGCTACTGTAC 422
Qy 121 rAla 122
Db 423 TGCT 426
RESULT 12
US-08-455-736-103
; Sequence 103, Application US/08455736
; Patent No. 5880328
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhans, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Sherice C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,736
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-1994
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566

; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION/DOCKET NUMBER: 36,129
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-455-736-103
Alignment Scores:
Pred. No.: 1,49e-35 Length: 653
Score: 335.50 Matches: 65
Percent Similarity: 72.13% Conservative: 23
Best Local Similarity: 53.28% Mismatches: 30
Query Match: 52.67% Indels: 4
Gaps: 1
US-09-786-715-2 (1-122) x US-08-455-736-103 (1-653)
Qy 2 AlagLugLugLgInValIleAlaGySHsLysIleAspGluTrpGluGlyInLeuGly 21
Db 72 TCCGAGAGGGAGCAAGTGTTCGGCTGCGCACAAAGTTGAGGAATGGAACGACTCTCAAG 131
Qy 22 LysTrpLysAspSerGluLysLeuValValAlaAspPheThrAlaSerTrpCysGlyPro 41
Db 132 AAGGGGTTGAGACTAAGAAACGCGTGTGATTTTACTCTTCATGCGTGGGSCCT 191
Qy 42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAlaPhe 61
Db 192 TCCCGTTTATTCCTCCCAATTCCTGACATTCCTAAGATGCCCCCATGTTATATTC 251
Qy 62 LeuLVaValAspValAspGluLeuAsnSerValAlaSer-LysTrpGluIleAsnAlaMe 81
Db 252 CTCAGAGTTGATGTGATGAGTGAAGACACTGTTTCACGGGAATGGAGTGTGAGGCAAT 311


```

Patent No. 6262342
GENERAL INFORMATION:
APPLICANT: Meins, Frederick
APPLICANT: Shinsht, Hideaki
APPLICANT: Wenzler, Herman
APPLICANT: Hofsteenge, Jan
APPLICANT: Rysals, John
APPLICANT: Speitsen, Christoph
TITLE OF INVENTION: DNA SEQUENCES ENCODING POLYPEPTIDES
TITLE OF INVENTION: HAVING BETA-1,3-GLUCANASE ACTIVITY
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6262342artis Corporation
STREET: 3054 Cornwallis Road, P.O. Box 12257
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,600
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/971,217
FILING DATE: 14-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,364
FILING DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667.
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018

```

```

FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/381,443
FILING DATE: 18-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/353,312
FILING DATE: 17-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/226,303
FILING DATE: 29-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-198250
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-350-600-103

Alignment Scores:
Pred. No.: 1,49e-35 Length: 653
Score: 335.50 Matches: 65
Percent Similarity: 72.13% Conservative: 23
Best Local Similarity: 53.28% Mismatches: 30
Query Match: 52.67% Indels: 4
DB: 3 Gaps: 1

US-09-786-715-2 (1-122) x US-09-350-600-103 (1-653)
QY 2 Alhgluglglglnvallealacyshtslvslleasplutrrpqluglglngluegly 21
Db 72 TCCGAGAGGAGGACAGAGTTCGGCTCCCAAGGTTGAGGAAAGCAAGCTTCAAG 131
QY 22 LysTrpLysAspSerGluLysLeuValValAspPheThrAlaSerTrpCysGlyPro 41
Db 132 AAGGCGGTGAGCACTAAGAAACGTCGTCGATTTTACCTCTTCATGTCGCGSCT 191
QY 42 CysArgAlaIleAlaProGlyrrPheThrGluLeuAlaLysAsnAsnProAsnValAlaPhe 61
Db 192 TGCCGTTTATTCGCCCAATTCCTTCGTCGATGCTAAGAAAGATGCCCATGTTATATTC 251
QY 62 LeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAlaHe 81
Db 252 CTCAGAGTTCATGTTATGATGACAGACGTTTCACGGGGAATGAGAGTGGAGCAAT 311
QY 81 tProthrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAspLy 101
Db 312 GCCAAGCTTTGCTTCATTAAAGATGGAAGAAAGAGGACAGAGTTCGTCGCAAGAA 371
QY 101 sValGlyLeuSerLysLysIleLeuGluLeuSerGlyThrThrProAlaIleThrSerh 121
Db 372 AGAGGAGTTCAGACAGACACATAGTGAAGATGCTGCT-----CCTGCTACTGTCAC 422
QY 121 rAla 122
Db 423 TGCT 426

RESULT 15
US-09-540-014-1
; Sequence 1, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: August 17, 2003, 19:25:47 ; Search time 142.207 Seconds
(without alignments)
1919.938 Million cell updates/sec

Title: US-09-786-715-2

Perfect score: 637
Sequence: 1 MAERGQYIACHKIDEMEGOL.....GLSKILELSTGPATSTA 122

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1504479 seqs, 1118970152 residues

Total number of hits satisfying chosen parameters: 3008958

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlp
-O=/cgn2_1/USPTO.spool/US09786715/runat_11082003_150515_6129/app_query.fasta_1_1052
-DB=Published.Applications_NA -OFMT=fastap -SUFFIX=trnph -MINMATCH=0.1
-LOOCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Blomsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pcot -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINTEN=0
-MAXLEN=2000000000 -USER=US09786715.ecgn_1_1_560.etrnat_11082003_150515_6129
-NCPU=6 -ICPU=3 -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100
-LONLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA:**

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PTCUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	377	59.2	3888	9	US-09-897-898-10 Sequence 10, Appl

2	376	59.0	345	10	US-09-938-842A-163	Sequence 163, App
3	376	59.0	3129	9	US-09-897-898-5	Sequence 5, Appl
4	376	59.0	3888	9	US-09-897-898-7	Sequence 7, Appl
5	360.5	56.6	402	10	US-09-878-574-3723	Sequence 3723, Ap
6	354	55.6	392	10	US-09-878-574-104	Sequence 104, App
7	345.5	54.2	360	10	US-09-938-842A-164	Sequence 164, App
8	343	53.8	390	10	US-09-878-574-1462	Sequence 1462, Ap
9	343	53.8	540	12	US-10-349-782-12	Sequence 12, Appl
10	323	50.7	357	10	US-09-938-842A-1736	Sequence 1736, Ap
11	323	50.7	357	14	US-10-323-362-1	Sequence 1, Appl
12	314	49.3	659	12	US-10-349-782-9	Sequence 9, Appl
13	302	47.4	369	12	US-10-194-885-8	Sequence 8, Appl
14	302	47.4	369	12	US-10-091-841-1	Sequence 1, Appl
15	298	46.8	392	12	US-10-091-841-3	Sequence 3, Appl
16	298	46.8	383	12	US-10-091-841-5	Sequence 5, Appl
17	274	43.0	260	10	US-09-878-574-12941	Sequence 12941, A
18	274	43.0	277	10	US-09-878-574-8135	Sequence 8135, Ap
19	263	41.3	272	10	US-09-878-574-8135	Sequence 8135, Ap
20	258	40.5	402	10	US-09-938-842A-225	Sequence 225, App
21	258	40.5	613	9	US-09-770-149-855	Sequence 855, App
22	257	40.3	268	10	US-09-878-574-5995	Sequence 5995, Ap
23	256	40.2	270	10	US-09-878-574-13445	Sequence 13445, A
24	252	39.6	456	10	US-09-924-035A-677	Sequence 677, App
25	250	39.2	250	9	US-09-923-876-1288	Sequence 1288, Ap
26	245	38.5	370	10	US-09-878-574-3169	Sequence 3169, Ap
27	232	36.4	413	11	US-09-918-995-6767	Sequence 6767, Ap
28	231	36.3	413	14	US-10-102-524-1396	Sequence 1396, Ap
29	231	36.3	418	10	US-09-796-692-3641	Sequence 3641, Ap
30	231	36.3	418	14	US-10-040-862-3641	Sequence 3641, Ap
31	231	36.3	464	10	US-09-998-598-1059	Sequence 1059, Ap
32	231	36.3	479	11	US-09-535-459-1145	Sequence 1145, Ap
33	231	36.3	536	14	US-10-066-543-65	Sequence 65, Appl
34	231	36.3	540	10	US-09-920-300A-1247	Sequence 1247, Ap
35	231	36.3	540	13	US-10-033-528-1247	Sequence 1247, Ap
36	231	36.3	557	10	US-09-884-441-88	Sequence 88, Appl
37	231	36.3	557	11	US-09-907-969-88	Sequence 88, Appl
38	231	36.3	557	14	US-10-198-053-88	Sequence 88, Appl
39	231	36.3	568	11	US-09-535-459-1139	Sequence 1139, Ap
40	231	36.3	570	11	US-09-535-459-1149	Sequence 1149, Ap
41	231	36.3	594	10	US-09-884-441-87	Sequence 87, Appl
42	231	36.3	594	11	US-09-907-969-87	Sequence 87, Appl
43	231	36.3	594	14	US-10-198-053-87	Sequence 87, Appl
44	231	36.3	601	10	US-09-884-441-133	Sequence 133, App
45	231	36.3	601	11	US-09-907-969-133	Sequence 133, App

ALIGNMENTS

RESULT 1
US-09-897-898-10
Sequence 10, Application US/09897898
Patent No. US20020037303A1
GENERAL INFORMATION:
APPLICANT: DECKERS, HARM M.
APPLICANT: VAN ROOIJEN, GIJS
APPLICANT: BOORHE, JOSEPH
APPLICANT: GOL, JANIS
APPLICANT: MOLONEY, MAURICE M.
TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
FILE REFERENCE: 034547/0104
CURRENT APPLICATION NUMBER: US/09/897, 898
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 09/577,147
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 09/448,600
PRIOR FILING DATE: 1999-11-24
PRIOR APPLICATION NUMBER: 09/084,777
PRIOR FILING DATE: 1998-05-27
PRIOR APPLICATION NUMBER: 60/047,753
PRIOR FILING DATE: 1997-05-27
PRIOR APPLICATION NUMBER: 60/047,779

; PRIOR FILING DATE: 1997-05-28
; PRIOR APPLICATION NUMBER: 60/075,863
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/075,864
; PRIOR FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 10
; LENGTH: 3888
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1555)..(2250)
; NAME/KEY: CDS
; LOCATION: (2491)..(2655)
; OTHER INFORMATION: Description of Unknown Organism: Phaseolin
; OTHER INFORMATION: promoter-trxn oleosin-phaseolin terminator
US-09-897-898-10

Alignment Scores:
Pred. No.: 2,2e-43 Length: 3888
Score: 377.00 Matches: 73
Percent Similarity: 71.67% Conservative: 13
Best Local Similarity: 60.83% Mismatches: 34
Query Match: 59.18% Indels: 0
DB: 9 Gaps: 0

US-09-786-715-2 (1-122) x US-09-897-898-10 (1-3888)

QY 2 AAGGCTAATGCAATCCAAACTCTTGTGCTGATTTCACGGCTTCTTGTGTGACCA 21
DB 1561 TCGGAAGAGAGCAAGATGATCGCTGCCACCGCTTGAGACATGGAACGAGCCTTCAG 1620
QY 22 LysTrpLysAspSerGluLysLeuValValAlaAspPheThrAlaSerTPCysGlyPro 41
DB 1621 AAGGCTAATGCAATCCAAACTCTTGTGCTGATTTCACGGCTTCTTGTGTGACCA 1680
QY 42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAlaPhe 61
DB 1681 TGTGCTTTCATCTGCTCATCTTGTGCTGATTTGGCTTAAGAACTTCTTAACGTGCTTTTC 1740
QY 62 LeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAlaMet 81
DB 1741 CTCAAGCTTCATCTGCTGATTTGAATGAAGTCGGTGCAGATGATTTGGCGATACAGCGCATG 1800
QY 82 ProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAspLys 101
DB 1801 CCAACCTTCATCTTGTGGAAGGAAGGAAGATTTTGGACAAGATTTTGGAGCCAGAAA 1860
QY 102 ValGlyLeuSerLysLysIleLeuGluLeuSerGlyThrThrProAlaAlaThrSerThr 121
DB 1861 GATGAGCTTCATCTGCTCATCTTGCACAACTTGGCTATGCGGATACAGCTAAGAGAAC 1920

RESULT 2
US-09-938-842A-163
; Sequence 163, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 163
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-163

Alignment Scores:
Pred. No.: 8,69e-45 Length: 345
Score: 376.00 Matches: 71
Percent Similarity: 77.57% Conservative: 12
Best Local Similarity: 66.36% Mismatches: 24
Query Match: 59.03% Indels: 0
DB: 10 Gaps: 0

US-09-786-715-2 (1-122) x US-09-938-842A-163 (1-345)

QY 2 AAGGCTAATGCAATCCAAACTCTTGTGCTGATTTCACGGCTTCTTGTGTGACCA 21
DB 7 TCGGAAGAGAGCAAGATGATCGCTGCCACCGCTTGAGACATGGAACGAGCCTTCAG 66
QY 22 LysTrpLysAspSerGluLysLeuValValAlaAspPheThrAlaSerTPCysGlyPro 41
DB 67 AAGGCTAATGCAATCCAAACTCTTGTGCTGATTTCACGGCTTCTTGTGTGACCA 126
QY 42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAlaPhe 61
DB 127 TGTGCTTTCATCTGCTCATCTTGTGCTGATTTGGCTTAAGAACTTCTTAACGTGCTTTTC 186
QY 62 LeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAlaMet 81
DB 187 CTCAAGCTTCATCTGCTGATTTGAATGAAGTCGGTGCAGATGATTTGGCGATACAGCGCATG 246
QY 82 ProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAspLys 101
DB 247 CCAACCTTCATCTTGTGGAAGGAAGGAAGATTTTGGACAAGATTTTGGAGCCAGAAA 306
QY 102 ValGlyLeuSerLysLysIle 108
DB 307 GATGAGCTTCATCTGCTCATCTTGCACAACTTGGCTATGCGGATACAGCTAAGAGAAC 327

RESULT 3
US-09-897-898-5
; Sequence 5, Application US/09897898
; Patent No. US200203703A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.
; APPLICANT: VAN ROOIJEN, GIJS
; APPLICANT: BOOTHIE, JOSEPH
; APPLICANT: GOLL, JANIS
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMATA, BIPIN K.
; TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
; FILE REFERENCE: 034547/0104
; CURRENT APPLICATION NUMBER: US/09/897,898
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/577,147
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/448,600
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/084,777
; PRIOR FILING DATE: 1998-05-27
; PRIOR APPLICATION NUMBER: 60/047,753
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: 60/047,779
; PRIOR FILING DATE: 1997-05-28
; PRIOR APPLICATION NUMBER: 60/075,863
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/075,864
; PRIOR FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 24

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3129
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1555)..(1896)
US-09-897-898-5

Alignment Scores:
Pred. No.: 2,23e-43 Length: 3129
Score: 376.00 Matches: 71
Percent Similarity: 77.57% Conservative: 12
Best Local Similarity: 66.36% Mismatches: 24
Query Match: 59.03% Indels: 0
DB: Gaps: 0

US-09-786-715-2 (1-122) x US-09-897-898-5 (1-3129)

QY 2 Aaagluglglgylgvallealacyshtslyslleasplutrpqluglgluengly 21
   ::::::::::::::::::::::::::::
DB 1561 TCGGAAGAAGCAAGATGATCCGCGCACACCGCTTGAGACATGGAAGCAGCAGCTTCAG 1620

QY 22 LysTrpLysAspSerGluLysLeuValValAlaAspPheThrAlaSerTrpCysGlyPro 41
   ||| ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1621 AAGGCTAATGAATCCAAACTCTTGtGGGTGATTCACGGCTTCTTGtGTGACCA 1680

QY 42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAspProAsnValAlaPhe 61
   ||||| ::::::::::::::::::::
DB 1681 TGTCCTTCATCGCCATTCCTTCTGCTGATTTGGCTAAGAACTCTTAACGCTGCTTTC 1740

QY 62 LeuLysValAspValAspGluLeuAsnSerValAlaIleSerLysTrpGluIleAsnAlaMet 81
   ||||| ::::::::::::::::::::
DB 1741 CTCGAAGTTGATCTGATGAATGAATGCGGTGGCAAGTGAATGGCGCTACAGCGCATG 1800

QY 82 ProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAspLys 101
   ||||| ::::::::::::::::::::
DB 1801 CCAACCTTCATCTTTTGAAGCAAGGAAGATTTGGACAAAGTTGTTGGACCAAGAAA 1860

QY 102 ValGlyLeuSerLysLysIle 108
   |||
DB 1861 GATGAGCTTCAGTCTACCATTT 1881

RESULT 4
US-09-897-898-7
; Sequence 7, Application US/09897898
; Patent No. US20020037303A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.
; APPLICANT: VAN ROOIJEN, GIJS
; APPLICANT: BOOTHE, JOSEPH
; APPLICANT: GOLL, JANIS
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMAI, BIRIN K.
; TITLE OF INVENTION: THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
; TITLE OF INVENTION: BODY BASED PRODUCTS
; FILE REFERENCE: 034547/0104
; CURRENT APPLICATION NUMBER: US/09/897,898
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/577,147
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/448,600
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/084,777
; PRIOR FILING DATE: 1998-05-27
; PRIOR APPLICATION NUMBER: 60/047,753
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: 60/047,779
; PRIOR FILING DATE: 1997-05-28
; PRIOR APPLICATION NUMBER: 60/075,863
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/075,864
```

```

; PRIOR FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 3888
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1555)..(1908)
; NAME/KEY: CDS
; LOCATION: (2149)..(2655)
; OTHER INFORMATION: Description of Unknown Organism: Phaseolin
; OTHER INFORMATION: promoter-oleosin Trxh-phaseolin terminator
US-09-897-898-7

Alignment Scores:
Pred. No.: 3.07e-43 Length: 3888
Score: 376.00 Matches: 71
Percent Similarity: 77.57% Conservative: 12
Best Local Similarity: 66.36% Mismatches: 24
Query Match: 59.03% Indels: 0
DB: Gaps: 0

US-09-786-715-2 (1-122) x US-09-897-898-7 (1-3888)

QY 2 Aaagluglglgylgvallealacyshtslyslleasplutrpqluglgluengly 21
   ::::::::::::::::::::::::::::::::::::
DB 2320 TCGGAAGAAGCAAGATGATCCGCGCACACCGCTTGAGACATGGAAGCAGCAGCTTCAG 2379

QY 22 LysTrpLysAspSerGluLysLeuValValAlaAspPheThrAlaSerTrpCysGlyPro 41
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 2380 AAGGCTAATGAATCCAAACTCTTGtGGGTGATTCACGGCTTCTTGtGTGACCA 2439

QY 42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAspProAsnValAlaPhe 61
   ||||| ::::::::::::::::::::
DB 2440 TGTCCTTCATCGCCATTCCTTCTGCTGATTTGGCTAAGAACTCTTAACGCTGCTTTC 2499

QY 62 LeuLysValAspValAspGluLeuAsnSerValAlaIleSerLysTrpGluIleAsnAlaMet 81
   ||||| ::::::::::::::::::::
DB 2500 CTCGAAGTTGATCTGATGAATGAATGCGGTGGCAAGTGAATGGCGCTACAGCGCATG 2559

QY 82 ProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAspLys 101
   ||||| ::::::::::::::::::::
DB 2560 CCAACCTTCATCTTTTGAAGCAAGGAAGATTTGGACAAAGTTGTTGGACCAAGAAA 2619

QY 102 ValGlyLeuSerLysLysIle 108
   |||
DB 2620 GATGAGCTTCAGTCTACCATTT 2640

RESULT 5
US-09-878-574-3723
; Sequence 3723, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: BYRUM, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3723
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-006-01-B1-F8
US-09-878-574-3723
```



```
Db      247 ATCCACACCTTGTGTTCATTAAGCGGCGAAGTTTGATAGCTGTTGCGAAT 306
QY      101 LysValGlyLeuSerLysLysIleuLeuSerGlyThrProAla 117
      307 AAAGAAGATCTTCAAGCGCAAAATAGTGAACATAGTGTGTACCACTGCG 357

RESULT 8
US-09-878-574-1462
; Sequence 1462, Application US/09878574
; Patent No. US2020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1462
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-037-01-B1-F11
US-09-878-574-1462

Alignment Scores:
Pred. No.:      5,86e-40      Length:      390
Score:          343.00      Matches:      64
Percent Similarity: 74.53%      Conservative: 15
Best Local Similarity: 60.38%      Mismatches:  27
Query Match:    53.85%      Indels:      0
DB:             10      Gaps:          0

US-09-786-715-2 (1-122) x US-09-878-574-1462 (1-390)
QY      3 GluGluGlyGlnValIleAlaCysHisLysIleAspGluTrpGluGlnLeuGlyLys 22
      69 GAAGAGGAGCAGATCGCGTCGATGAGTGAAGTGCACACTGCACAGAT 128
QY      23 TrpLysAspSerGlyLysLeuValValAlaAspPheThrAlaSerTrpCysGlyProCys 42
      129 GCAAAAGACTCCAAAATACTGATGTGTGGATTTTACGCTTCTCGTGTGCTCATGC 188
QY      43 ArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAlaPheLeu 62
      189 CGTTTATGCGCCCGCACTTCTTCAGAGATTGCAGAAAGAAATCTCGAATTGATCTCTC 248
Db      63 LysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAlaMetPro 82
      249 AAAGTGAGTGTGAAGTGAAGGCGCTGTGCTGAGAAATATTCATTGAGGCATGCCA 308
QY      83 ThrPheValPheLeuLysGlyLysIleIleGluLysIleValGlyAlaAspLysVal 102
      309 ACCTTCCTCTTCTTTAAAGATGCGCAGATGCTGACAGAGGTGCTGTAGTAAGAT 368
Db      103 GlyLeuSerLysLysIle 108
      369 GACCTTCAACGACCATTA 386

RESULT 9
US-10-349-782-12
; Sequence 12, Application US/10349782
; Publication No. US20030143618A1
; GENERAL INFORMATION:
; APPLICANT: Yves Hatzfield
; APPLICANT: Valerie Marie-No. US20030143618A1lle Frankard
; APPLICANT: Anne-Marie Droual
; TITLE OF INVENTION: Method for easy cloning and selection of chimeric DNA molecules
; FILE REFERENCE: 1187-15
```

```
; CURRENT APPLICATION NUMBER: US/10/349,782
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: EP 02075373.7
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 540
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified thioredoxin of Oryza sativa in vector pDONR201
US-10-349-782-12

Alignment Scores:
Pred. No.:      9.46e-40      Length:      540
Score:          343.00      Matches:      66
Percent Similarity: 69.75%      Conservative: 17
Best Local Similarity: 55.46%      Mismatches:  36
Query Match:    53.85%      Indels:      0
DB:             12      Gaps:          0

US-09-786-715-2 (1-122) x US-10-349-782-12 (1-540)
QY      2 AlaGluGlyGlnValIleAlaCysHisLysIleAspGluTrpGluGlnLeuGlyLys 21
      64 GCCAGAGAGGAGTGTGATCGCTGCCCAACAAGACGAGCTGACGCCCGAGAGACC 123
Db      64 GCGAGAGAGGAGTGTGATCGCTGCCCAACAAGACGAGCTGACGCCCGAGAGACC 123
QY      22 LysTrpLysAspSerGlyLysLeuValValAlaAspPheThrAlaSerTrpCysGlyPro 41
      124 AAGGCCAAGAGAGCGCGCAAAAGTGTGATTAATGACTTACGCTTCTCGTGTGCGGACCG 183
QY      42 CysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAlaPhe 61
      184 TGCCTTCATCGCCCGCACTGCTCGTGAATACGCCCAAAAGTTCCTGCTGCTCTTC 243
Db      62 LeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAlaMet 81
      244 CTGAAGCTTGATGTGATGATGCTGAAGAGATGCTCGAAGAAATACAAATGCGAGCAAG 303
QY      82 ProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAspLys 101
      304 CCGACCTTCCTATTCATCAAGATGATGCTGAGGCTGACAAAGTGTGCGCCAGAGAG 363
Db      102 ValGlyLeuSerLysLysIleLeuGluLeuSerGlyThrThrProAlaIleThrSer 120
      364 GATGACCTTCAGAACACATCGTGAAGCAGCTGCGTGCATCTGCTCTCT 420

RESULT 10
US-09-938-842A-1736
; Sequence 1736, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCDP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1736
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 19:20:27 ; Search time 1649.9 Seconds
(without alignments)
1797.162 Million cell updates/sec

Title: US-09-786-715-2
Perfect score: 637
Sequence: 1 MAEQQVACHKIDWEGQL.....GLSKILELSTTPATSTA 122

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 segs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+2n model -DEV=xlp
-O=/ggn2.1/USPTO/US09786715/runat_11082003_150514_6048/app.query.fasta_1.1052
-DB=EST -QFMT=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPEXT=0
-ONITS=bits -STAR=1 -END=-1 -MATRIX=blomsu62 -TRANS=human4.0.cdi -LIST=45
-DOCLIGN=200 -THR.SCORE=Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=nto -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09786715_@CGN_1.1.7834_@runat_11082003_150514_6048 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOC
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: em_estba:*
2: em_estcha:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hrc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_fut:*
21: em_gss_fut:*
22: em_gss_mam:*
23: em_gss_mam:*
24: em_gss_pro:*
25: em_gss_pro:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred.. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	390.5	61.3	622	9	AW255457
2	385	60.4	487	13	B0878216
3	385	60.4	538	9	A1161830
4	385	60.4	568	13	B0866690
5	385	60.4	610	13	B0836847
6	385	60.4	611	14	CA821710
7	385	60.4	612	13	B0888094
8	385	60.4	641	13	B0830685
9	385	60.4	641	13	B0873533
10	383	60.1	520	13	B0885783
11	383	60.1	523	13	B0812532
12	383	60.1	523	13	B0829684
13	383	60.1	531	12	B1136756
14	383	60.1	532	13	B0884977
15	383	60.1	544	13	B0827985
16	383	60.1	555	13	B0885050
17	383	60.1	557	13	B0886021
18	383	60.1	579	13	B0876591
19	383	60.1	591	13	B0884811
20	383	60.1	594	13	B0837287
21	383	60.1	600	13	B0884129
22	383	60.1	601	13	B0895406
23	383	60.1	670	13	B0868860
24	382.5	60.0	602	10	BE054543
25	382	60.0	492	12	B1126457
26	382	60.0	495	12	B1124724
27	382	60.0	507	12	B1124769
28	382	60.0	534	12	B1124332
29	382	60.0	560	12	B1126407
30	382	60.0	611	13	B0872611
31	381	59.8	541	14	CA823905
32	381	59.8	591	14	CA826440
33	379	59.5	397	13	B0816912
34	379	59.5	461	12	B1125905
35	379	59.5	467	13	B0818910
36	379	59.5	485	13	B0818945
37	379	59.5	570	12	B1126033
38	379	59.5	588	14	CB185215
39	379	59.5	603	13	B0874273
40	379	59.5	606	13	B0408049
41	379	59.5	622	14	CB239393
42	378.5	59.4	658	13	B0874439
43	378.5	59.4	455	9	A1773303
44	378.5	59.4	477	9	AM041395
45	378.5	59.4	505	9	AM094525

ALIGNMENTS

RESULT 1
AM255457
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW255457 622 bp mRNA linear EST 23-AUG-2000
M1480 peppermint glandular trichome Mentha x piperita CDNA, mRNA
sequence.
AW255457.1 GI:7244709
EST.
Mentha x piperita (peppermint)
Mentha x piperita
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Lamiaceae; Nepetoideae; Menthae;

REFERENCE	TITLE	AUTHORS
1 (bases 1 to 622)	Mentha.	
Lange,B.M., Wildung,M.R., Stauber,E.J., Sanchez,C., Pouchnik,D. and Croteau,R.		
	Probing essential oil biosynthesis and secretion by functional evaluation of expressed sequence tags from mint glandular trichomes	
Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2934-2939 (2000)		
JOURNAL MEDLINE		
20183992		
PUBMED		
10717007		
COMMENT		
	Contact: Lange, B.M	
	Institute of Biological Chemistry/Washington State University	
	Pulman, WA	
	Email: lange-m@mail.wsu.edu.	
FEATURES		
source		
	1..622	
	/organism="Mentha x piperita"	
	/mol_type="mRNA"	
	/culivar="Black Mitcham"	
	/db_xref="taxon:34236"	
	/tissue_type="petalate glandular trichomes"	
	/cell_type="secretory"	
	/clone_lib="peppermint glandular trichome"	
	/note="Vector: lambda ZAP"	
BASE COUNT		
ORIGIN		
	192 a 129 c 143 g 158 t	
Alignment Scores:		
Pred. NO.:	7.16e-40	Length: 622
Score:	390.50	Matches: 77
Percent Similarity:	73.95%	Conservative: 11
Best Local Similarity:	64.71%	Mismatches: 28
Query Match:	61.30%	Indels: 3
Db:	9	Gaps: 1
US-09-786-715-2 (1-122) x AW255457 (1-622)		
Oy	4	gluclglnvalallealaacyshtlaileaspcltrpglgnleuglylvsrtip 23
Db	65	GAAGACAGGATCGGCTGCCACACACGATACCTGGAAACGACGCTTCAGAAAGCG 124
Oy	24	lyssaspserglulysleuvalvalaspbetherlasertrpccysgylprocyarg 43
Db	125	AATGATTAACAAGAGGTGGTGGTGGATTCCTCTCTCTGTCGGACCTGTCGG 184
Oy	44	Alallelaaprotyrpethrthglulenalalysansnproasvalalaphleuyls 63
Db	185	TTTCATCGCTCATTTCTTCCGACGAAATTCGACAAAGATTCCTTAATGACATTTCTAAG 244
Oy	64	valaspvalaspgluleuasnservalaaserlystrpqlulaaenalamelprothr 83
Db	245	GTGGATGTCGATGAGTTGGAAGTCGGTGTGACGTGACGTGGGACGGAATGCCAAC 304
Oy	84	phetaalpheleuylslyllyllellelglulysllevalglylaasplysvalgly 103
Db	305	TTTCATTTCTCTCAAAAGAGGAAATTTTGACAGACGTCTGGGACGGAAGAAAGAGAG 364
Oy	104	leuserlysylsileuugluleusergylthtrhrproalaiaithrrsertthala 122
Db	365	CTGCAGCAATATATCTCTAAGCACCTCAACACA-----GCTACTAGTACTGCT 412
RESULT 2		
LOCUS	B0878216	487 bp mRNA linear EST 16-OCT-2002
DEFINITION	V044E02 Populus flower cDNA library Populus balsamifera subsp.	
ACCESSION	B0878216	trichocarpa cDNA 5 prime, mRNA sequence.
VERSION	B0878216.1	GI:24069740
KEYWORDS	EST.	
SOURCE	Populus balsamifera subsp. trichocarpa	
ORGANISM	Populus balsamifera subsp. trichocarpa	
	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;	
	Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: rosids	
	; eucotsids I; Malpighiales; Salicaceae; Populus.	

REFERENCE	1 (bases 1 to 487)
AUTHORS	Umeberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
TITLE	The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
JOURNAL	Unpublished
COMMENT	Contact: BHALERAO RUPALI R. Umae Plant Science Center Department of Plant Physiology University of Umea, 901 87 Umea, Sweden Tel: +46 90 786 5279 Fax: +46 90 786 6676 Email: rupali.bhalerao@plantphys.umu.se.
FEATURES	Location/Qualifiers
SOURCE	1..487
	/organism="Populus balsamifera subsp. trichocarpa"
	/mol_type="mRNA"
	/sub_species="trichocarpa"
	/db_xref="taxon:3694"
	/clone_lib="Populus flower cDNA library"
	/note="Organ: flower"
BASE COUNT	130 a 80 c 127 g 150 t
ORIGIN	
Alignment Scores:	
Pred. No.:	2.63e-39
Score:	385..00
Percent Similarity:	78.85%
Best Local Similarity:	67.31%
Query Match:	60.44%
DB:	13 Gaps: 0
US-09-786-715-2 (1-122) x BU878216 (1-487)	
OY	1 MetaIaGIuGluGIyGIuValIIleAlaCySHsLySIleAspGluTrpGluclyInLeu 20
Db	33 ATGGCCGAGAGAAGACCAAGTATTGCCCGCACACAGTGAGATACCTGGAAAGACATTTC 92
OY	21 GIyLSTrPpLYASpSerGILuLSyLeuValValAAspPhetHAlASerTPcyScLy 40
Db	93 GAGAAAGGGAAGGCTGCAGAAACTGTGATTCGGGATTTTACGCTTCATGGTGCCA 152
OY	41 ProCysArGaIAIleAlaProTyPheThrcIGluLeuAlaLyASnAsnProAsnValAla 60
Db	153 CCATGTAAATAGATTGCTCCCATCTTCGCCCGAGTTGGGAGAAAGTTCCCAATGTACA 212
OY	61 PHeLeuLySVAlAspValAspGLuleuAsnSeRValAlASerLySTrPGluILEasnaLa 80
Db	213 TTCCTGAAGGGATGTGATGAAATTGAAGCGCTGTCTGAGAGTGAATGTGAGGCA 272
OY	81 MeTrProThrPHeValPHeLeuLySGlyLySIleIEgluLySIleValGIyAlAAsp 100
Db	273 ATGCCAACCTTATTTCCTCTGAAGAGTGGAAAATTAGTGCACAAACCTGTGGTCTGAT 332
OY	101 LySVAlGIyLeu 104
Db	333 AAGATGGCGCTG 344
RESULT 3	
LOCUS	At161830 538 bp mRNA linear EST 03-DEC-1998
DEFINITION	A007P520 Hybrid aspen plasmid library Populus tremula x Populus tremuloides cDNA 5', mRNA sequence.
ACCESSION	At161830
VERSION	At161830.1 GI:3853115
KEYWORDS	EST.
SOURCE	Populus tremula x Populus tremuloides
ORGANISM	Populus tremula x Populus tremuloides
REFERENCE	Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta; eudicotyledons: core eudicots: rosids 1 (bases 1 to 538)
AUTHORS	A., Amil,B., Bhalerao,R., Larsson,M., Villarroel,R., Van Montagu

M., Sandberg, G., Olsson, O., Teeri, T., Boerjan, W., Gustafsson, P., Uhlen, M., Sundberg, B., and Lundberg, U.
Gene discovery in the wood-forming tissues of poplar: Analysis of 5,692 expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)

COMMENT

9789088
Contact: Sterky F
Department of Biotechnology
Royal Institute of Technology (KTH)
Teknikringen 34, S-100 44 STOCKHOLM, Sweden
Tel: +46 8 790 8287
Fax: +46 8 24 54 52
Email: fredrik@biochem.kth.se
PCR Primers
FORWARD: AAGGGGATGCTGCGCAAGCG
BACKWARD: GCTTCCGCTGCTGATGTTGTGTG
Seq primer: CGTTGTAACGACGCGCCAG
High quality sequence stop: 538.
Location/Qualifiers

FEATURES

source

1..538
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue_type="Cambial region"
/dev_stage="1.5 m actively growing tree"
/lab_host="E.coli"
/clone_lib="Hybrid aspen plasmid library"
/note="Vector: pBluescript SK; Site_1: SalI; Site_2: NotI; Cambial region tissues, including developing xylem, the meristematic cambial zone and the developing and mature phloem, was harvested from 1.5 m actively growing trees. cDNA was prepared and cloned into lambda gt22a. DNA was isolated and subcloned into pBluescript SK using SalI and NotI restriction enzymes."

BASE COUNT 140 a 90 c 152 g 148 t 8 others
ORIGIN

Alignment Scores:

Pred. No.: 3,01e-39 Length: 538
Score: 385.00 Matches: 70
Percent Similarity: 78.85% Conservative: 12
Best Local Similarity: 67.31% Mismatches: 22
Query Match: 60.44% Indels: 0
DB: 9 Gaps: 0

US-09-786-715-2 (1-122) x A1161830 (1-538)

QY 1 MetAtAGlUGlUGlNValIleAlaCySHisLysIleAspGluTrpGluGlnLeu 20
|||||
DB 30 ATGCCGAAAGAGCAAGTTATTCCTGCCACACAGATGATCCTGGAAAGCATTTTC 89
QY 21 GlyLSTPrLysASpSerGluLysLeuValValAspPheThrAlaSerTrpCysGly 40
|||
DB 90 GAGAAGGGAAGAGGCTTCAGAAAGTGTGCGGATTTTACGCTTCACAGGTGTCCA 149
QY 41 ProCysArgAlaIleAlaProTyrPheThrGluLeuValAlaSerLysTrpGluLeu 60
|||||
DB 150 CCATATAAATGATTTGCTCCATCTTCGCCGCGAGTGGCGAAGCATTTCTTAATGTACA 209
QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluLeu 80
|||||
DB 210 TTCTGAAGGTGATGATGATGATGAAGCTGTGCTGAGAGATGGATGTGAGGCA 269
QY 81 MetProThrPheValPheLeuLysGlyLysIleIleGluLysIleValGlyAlaAsp 100
|||||
DB 270 ATGCCAAGCTTTATTTCTCTGAAGATGAAAAATAGTGACAAACTGTGGTGTCTGAT 329
QY 101 LysValGlyLeu 104
|||
DB 330 AAGATGCTCTG 341

RESULT 4

B0866690
LOCUS B0866690 568 bp mRNA linear EST 16-OCT-2002
DEFINITION S069F05 Populus imbed seed cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.

ACCESSION B0866690
VERSION B0866690.1 GI:24057344.
KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides

REFERENCE 1 (bases 1 to 568)
Umeberg, P., Bhalerao, R., Jansson, S., and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries

JOURNAL

Unpublished
Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.

FEATURES

source

1..568
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue_type="Imbed seed"
/clone_lib="Populus imbed seed cDNA library"

BASE COUNT 147 a 90 c 149 g 182 t
ORIGIN

Alignment Scores:

Pred. No.: 3.24e-39 Length: 568
Score: 385.00 Matches: 70
Percent Similarity: 78.85% Conservative: 12
Best Local Similarity: 67.31% Mismatches: 22
Query Match: 60.44% Indels: 0
DB: 13 Gaps: 0

US-09-786-715-2 (1-122) x B0866690 (1-568)

QY 1 MetAtAGlUGlUGlNValIleAlaCySHisLysIleAspGluTrpGluGlnLeu 20
|||||
DB 42 ATGCCGAAAGAGCAAGTTATTCCTGCCACACAGATGATCCTGGAAAGCATTTTC 101
QY 21 GlyLSTPrLysASpSerGluLysLeuValValAspPheThrAlaSerTrpCysGly 40
|||
DB 102 GAGAAGGGAAGAGGCTTCAGAAAGTGTGCGGATTTTACGCTTCACAGGTGTCCA 161
QY 41 ProCysArgAlaIleAlaProTyrPheThrGluLeuValAlaSerLysTrpGluLeu 60
|||||
DB 162 CCATATAAATGATTTGCTCCATCTTCGCCGCGAGTGGCGAAGCATTTCTTAATGTACA 221
QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluLeu 80
|||||
DB 222 TTCTGAAGGTGATGATGATGATGAAGCTGTGCTGAGAGATGGATGTGAGGCA 281
QY 81 MetProThrPheValPheLeuLysGlyLysIleIleGluLysIleValGlyAlaAsp 100
|||||
DB 282 ATGCCAAGCTTTATTTCTCTGAAGATGAAAAATAGTGACAAACTGTGGTGTCTGAT 341
QY 101 LysValGlyLeu 104
|||
DB 342 AAGATGCTCTG 353

RESULT 5
B0836847 610 bp mRNA linear EST 15-OCT-2002
LOCUS B0836847
DEFINITION T091F03 Populus apical shoot cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.

ACCESSION B0836847
 VERSION B0836847.1 GI:24019659
 KEYWORDS EST
 SOURCE Populus tremula x Populus tremuloides
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucosids I; Malpighiales; Salicaceae; Populus.
 REFERENCE 1 (bases 1 to 610)
 AUTHORS Uneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
 JOURNAL Unpublished
 COMMENT Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 FEATURES
 source location/Qualifiers
 1..610
 /organism="Populus tremula x Populus tremuloides"
 /mol_type="mRNA"
 /db_xref="taxon:47664"
 /tissue_type="apical shoot"
 /clone_lib="Populus apical shoot cDNA library"
 BASE COUNT 153 a 95 c 160 g 202 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.57e-39 Length: 610
 Score: 385.00 Matches: 70
 Percent Similarity: 78.85% Conservative: 12
 Best Local Similarity: 67.31% Mismatches: 22
 Query Match: 60.44% Indels: 0
 Gaps: 0
 DB: 13
 US-09-786-715-2 (1-122) x B0836847 (1-610)
 QY 1 MetAlaGlUGlUGlGlnValIleAlaCySHisLysIleAspLutrrpGlnGlnLeu 20
 Db 34 ATGGCCGAAGAAAGCAAGTATTGCTGCTGCACACAGTGATACCTGGAAAGCATTTTC 93
 QY 21 GilystrPlpLysAspserGluLysLeuValValAlaSpPheThrAlaSerTPCySgLy 40
 Db 94 GAGAAAGGAAAGGCGCTCGAAGAACGATGTGCTGATTTTCTGCTTCATGTGTCCA 153
 QY 41 ProCysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAla 60
 Db 154 CCATGTAAATGATTCCTCCATCTCGCCGAGCTGGCGAAGATTTCTTATGTGCACA 213
 QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
 Db 214 TTCTTTAAGGTGATGTGATGATGAATGAAGCGCTGTCGAGAGTGAATGGAGCGCA 273
 QY 81 MetProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAsp 100
 Db 274 ATGCCCAACTTTATTTCTCGAAAGATGGAATTTAGTGCACAAACTGTGGTCTGTGAT 333
 QY 101 LysValGlyLeu 104
 Db 334 AAAGATGCTCTG 345
 RESULT 6
 CA821710 611 bp mRNA linear EST 28-FEB-2003
 LOCUS RSH06D10 two-month-old roots from clone 'Beaupre' grown for 19 days
 DEFINITION under restricted irrigation Populus balsamifera subsp. trichocarpa
 x Populus deltoides cDNA 5', mRNA sequence.
 ACCESSION CA821710.1 GI:28605259
 VERSION EST.
 KEYWORDS

SOURCE Populus balsamifera subsp. trichocarpa x Populus deltoides
 ORGANISM Populus balsamifera subsp. trichocarpa x Populus deltoides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucosids I; Malpighiales; Salicaceae; Populus.
 REFERENCE 1 (bases 1 to 611)
 AUTHORS Kohler, A., Delaruelle, C., Martin, D. and Martin, F.
 TITLE The poplar root transcriptome: analysis of 6000 expressed sequence tags
 JOURNAL Unpublished (2002)
 COMMENT Contact: Martin FM
 Equipe de Microbiologie Forestiere
 Institut National de la Recherche Agronomique
 Centre INRA de Nancy, 54280 Champenoux, France
 Tel: +33 383 39 40 80
 Fax: +33 383 39 40 69
 Email: fmartin@nancy.inra.fr
 Insert Length: 611 Std Error: 0.00
 Seq primer: Fornat 5' AAGCGCCGCTGTGTGTGATCCC.
 FEATURES
 source location/Qualifiers
 1..611
 /organism="Populus balsamifera subsp. trichocarpa x Populus deltoides"
 /mol_type="mRNA"
 /cultivar="Beaupre/"
 /db_xref="taxon:3695"
 /dev_stage="two-month-old"
 /clone_lib="two-month-old roots from clone 'Beaupre' grown for 19 days under restricted irrigation"
 /note="Organ: root; Vector: pTrioLex2; cDNA library of roots from two-month-old Populus trichocarpa Torr. & Gray x deltoides Bart. Ex Marshall (clone 'Beaupre') grown for 19 days under restricted irrigation to reach 50% of the transpiration rate of fully watered plants. The cDNA library was constructed from 1 ug of total RNA using the SMART cDNA synthesis kit (Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. The resulting cDNA was packed into lambda phages using the GigaPack III Gold packaging kit (Stratagene, La Jolla, CA). The pTrioLex2 phagemid clones in Escherichia coli were obtained by using the mass in vivo excision protocol according to the manufacturer's instructions (Clontech)."
 BASE COUNT 161 a 97 c 159 g 190 t 4 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.58e-39 Length: 611
 Score: 385.00 Matches: 70
 Percent Similarity: 78.85% Conservative: 12
 Best Local Similarity: 67.31% Mismatches: 22
 Query Match: 60.44% Indels: 0
 Gaps: 0
 DB: 14
 US-09-786-715-2 (1-122) x CA821710 (1-611)
 QY 1 MetAlaGlUGlUGlGlnValIleAlaCySHisLysIleAspLutrrpGlnGlnLeu 20
 Db 58 ATGGCCGAAGAAAGCAAGTATTGCTGCTGCACACAGTGATACCTGGAAAGCATTTTC 117
 QY 21 GilystrPlpLysAspserGluLysLeuValValAlaSpPheThrAlaSerTPCySgLy 40
 Db 118 GAGAAAGGAAAGGCGCTCGAAGAACGATGTGCTGATTTTCTGCTTCATGTGTCCA 177
 QY 41 ProCysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnAsnProAsnValAla 60
 Db 178 CCATGTAAATGATTCCTCCATCTCGCCGAGTGGCAAGATTTTCCCATGTCACA 237
 QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
 Db 238 TTCTTTAAGGTGATGTGATGATGAAGCGCTGTGCTGAGAGAGTGAATGTGGAGCGCA 297
 QY 81 MetProThrPheValPheLeuLysLysGlyLysIleIleGluLysIleValGlyAlaAsp 100

DB	LOCUS	SEQUENCE	FROM	PATENT	DNA	LINEAR	PAT	DATE
Db	175192	Sequence 103 from patent US 5689044.						
RESULT 11	175192	GI:3011333						
LOCUS	175192	GI:3011333						
ACCESSION	175192							
VERSION	175192.1							
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unknown.							
REFERENCE	Unclassified.							
AUTHORS	1 (bases 1 to 653)							
TITLE	Ryals, J.A., Friedrich, L.B., Oknes, S.J. and Ward, E.R.							
JOURNAL	Chemically inducible promoter of a plant PR-1 gene							
FEATURES	Patent: US 5689044-A 103 18-NOV-1997;							
source	Location/Qualifiers							
	1..653							
BASE COUNT	165 a	114 c	157 g	215 t	2 others			
ORIGIN	/organism="unknown"							
Alignment Scores:								
Pred. No.:	8.84e-48	Length:	653					
Score:	473.50	Matches:	90					
Best Similarity:	88.33%	Conservative:	16					
Best Local Similarity:	75.00%	Mismatches:	10					
Query Match:	78.01%	Indels:	4					
DB:	6	Gaps:	1					
US-09-786-715-4 (1-118) x 175192 (1-653)								
QY	3	SerserGIugIugIugIugIugIValIIleGIYCyshISserValaSPglUTrPLySglUlnPhe	22					
Db	69	TCATCCGAGGAGGGGCAAGGTGTGGCGGCCACAAAGTGAAGATGGAAGAGTACTTC	128					
QY	23	GLInySGIValaSPserLySLySLyValValIIleasPheThrAlaSerTPCySGLY	42					
Db	129	AAGAAGGCGGTGAAGACTAAGAAGCTGGTGGTGCATTTTACTGCTTCATGGTGGCGS	188					
QY	43	ProCYaSPheIIleAlaProlIleuValIuetaIaLySLyThPProISValIle	62					
Db	189	CCTTGCGCTTTATATGCCCAATCTCTGCTACATTCGTAGAAGATGCCCATGTTATA	248					
QY	63	PheIeuLySLaSPValaSPGLySLySLyThValAla-glUlnPheLySLaIuAl	82					
Db	249	TTCTCAAGCTGTGATGTGATGAACCTGTTCCAGCGGAATGAGATGTGAGGC	308					
QY	82	aMetPProThrPheValPheIeuLySLySLySLyValIuValIuValIuValIuAla	102					
Db	309	AATGCCAATTTTGTCTTCAATTAAAGATGGAAGAAAGTGGACAGAGTGTGGTGGCA	368					
QY	102	gLySGIuGLySLySLySLyValIuValIuValIuValIuValIuValIuValIuValIu	118					
Db	369	GAAAGAGAGGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	426					
RESULT 12	AV170650	665 bp	mrna	linear	PLN 02-JAN-2003			
LOCUS	AV170650	665 bp	mrna	linear	PLN 02-JAN-2003			
DEFINITION	Pisum sativum clone 3 thiorodoxin h mRNA, complete cds.							
ACCESSION	AV170650							
VERSION	AV170650.1							
KEYWORDS	GI:27466893							
SOURCE	Pisum sativum (pea)							
ORGANISM	Pisum sativum							
REFERENCE	Unclassified.							
AUTHORS	1 (bases 1 to 665)							
TITLE	Montrichard, F., Renard, M., Duval, F.D. and Machereel, D.							
	Expression of the NADP-thioredoxin reductase/thioredoxins h system							

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

unpublished during germination of seeds of *Pisum sativum* L
2 (bases 1 to 665)
MontRichard, F., Renard, M., Duval, F. D. and Macherel, D.
Direct Submission
Submitted (30-OCT-2002) UMR 1191 Physiologie Moléculaire des
Semences, UFR Sciences, 16 bd Lavoisier, Angers 49045, France

FEATURES
source
location/qualifiers
1..665
/organism="Pisum sativum"
/mol_type="mRNA"
/db_xref="taxon:3888"
/clone="3"
74..415
/note="trix h"
/codon_start=1
/product="thioredoxin h"
/protein_id="AA012854.1"
/db_xref="GI:27466894"
/translation="MAEEGVIGVHTVDAMKEOLEKSKKLIVDFTASMGCPERR
IAPLRIAKTKLHTVFLKVDVDELKTVSEEMGLEAMPTEFLKDGELVDKVVAKKE
ELQKIKRHA"

BASE COUNT
ORIGIN
220 a 85 c 164 g 196 t

Alignment Scores:
Score: 3.25e-44 Length: 665
Percent Similarity: 444.00 Matches: 81
Percent Similarity: 88.39% Conservative: 18
Best Local Similarity: 72.32 Mismatches: 13
Query Match: 73.15% Indels: 0
DB: 8 Gaps: 0

US-09-786-715-4 (1-118) x AY170650 (1-665)

Oy 4 SerGIuGluGluGluValIIleGLYCyHISserValAspGIuTrpGluGluInPhagIn 23
Db 77 GCGGAAGAGGGACAGTgATCGtTGtCACACCGTGGCTTGtGAAGAAGACAGTTAG 136
Oy 24 LysGIyValAspSerLysLysLeuValValIIleAspPheThrAlaSerTrpCyGlyPro 43
Db 137 AAGGAAAGCCCTCAAGAAACAGTATGTGATGATTTCACCTCTTGtGGCGGCCA 196
Oy 44 CysArpPheIIleAlaProIIleLeuAlaGluMetAlaLysLysTrpProHISValIIlePhe 63
Db 197 TGCCGTTTATTTGGCCCAATTTTGGCAGAGATTCCTAAAGAGCTTACACATGTCATTTC 256
Oy 64 LeuLysValAspValAspGIuLeuLysThrValAlaGluGluPheLysValGluAlaMet 83
Db 257 CTTAAGGTTCACGTGATGATTAAGACGTCTTCCAGAGAGTGGGCAATTAAGACGTATG 316
Oy 84 ProThrPheValPheLeuLysGluGlyLysGIuValGluArgLeuValGlyAlaArgLys 103
Db 317 CCACATTCCTGTTCTTGAAAGAGTGGAGCACTTGtGCAAAAGTTGGGTGCCAAGAG 376
Oy 104 GluGluLeuGluAlaThrValGluLysHISGlyAla 115
Db 377 GAGGAGCTGCATTTGAAAATTGACACACATGCACGCT 412

RESULT 13
RCHTHORXN
LOCUS 603 bp mRNA linear PLN 04-APR-1996
DEFINITION R. communis mRNA for thioredoxin.
ACCESSION 270677
VERSION 270677.1 GI:1255953
KEYWORDS thioredoxin.
SOURCE R. communis (castor bean)
ORGANISM R. communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
1 (bases 1 to 603)
Szederkényi, J., Doljener, E. and Schobert, C.

BASE COUNT 165 a 114 c 157 g 215 t 2 others
 ALIGNMENT SCORES:
 Pred. No.: 8,84e-48 Length: 653
 Score: 473.50 Matches: 90
 Percent Similarity: 88.33% Conservative: 16
 Best Local Similarity: 75.00% Mismatches: 10
 Query Match: 78.01% Indels: 4
 Gaps: 1

US-09-786-715-4 (1-118) x I38524 (1-653)

QY 3 SerSerGIUGLUGLInValIleGIYcYshISserValAspGIUTrPlySGluInPhe 22
 ||||| 69 TCATCCGAGGAGGCAAGTGTTCGCTGCCCAAGAGTTGAGAAATGAGACGACTTC 128
 ||||| 23 GlnIysGIyValAspSerLysLysLeuValAlIleAspPheThrAlaSerTrpCysGly 42
 ||||| 129 AAGAAAGCGTTGAGACTAAGAACTGGTGGTGCATTTTACTGCTTCATGAGTGGCGS 188
 ||||| 43 ProCysArgPheIleAlaProIleuAlaGluMetAlaLysThrProHisValIle 62
 ||||| 189 CCTTGCCTTTATTATGCCCCCAATTCCTGCTGACATGCTTAAGAAAGATGCCCATGTATTA 248
 ||||| QY 63 PheLeuLysValAspValAspGIUleuLysThrValAla-GluGIUphelYsValGIUAl 82
 ||||| Db 249 TTCCTCAAGGTTGATGTGATGAAGTGTTCACGCGGAAATGAGAGTGGAGGC 308
 ||||| QY 82 aMetProThrPheValPheLeuLysGIUGLysGIUValGIUArgLeuValGIYAlaAr 102
 ||||| Db 309 AATGCCAACTTTTCTTCATTAAGAGGAAAGAGTGGCAAGAGTGGTGGCGCA 368
 ||||| QY 102 gLySGluGIUleuGlnAlaThrValGIUlyshISGIYAla-----IleThrAla 118
 ||||| Db 369 GAAAGAGAGTTTGCAGCAGACCATATGTAAGACATCTCTCTCTACTGTACTGCT 426
 |||||

RESULT 9
 156999 LOCUS I56999 Sequence 103 from patent US 5650505.
 156999 DEFINITION I56999
 156999 VERSION I56999.1 GI:2477412
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 653)
 AUTHORS Ryals,J.A., Alexander,D.C., Beck,J.J., Duesing,J.H., Goodman,R.M.,
 Friedrich,L.B., Harms,C., Meins,F., Jr., Montoya,A. deceased,
 Meyer,M.B., Neuhaus,J.-M., Payne,G.B., Spertsen,C., Stinson,J.R.,
 Ukres,S.J., Ward,E.R. and Williams,S.C.
 TITL Chemically regulatable and anti pathogenic DNA sequences and uses
 JOURNAL Patent: US 5650505-A 103 22-JUL-1997;
 FEATURES location/Qualifiers
 source 1..653
 BASE COUNT 165 a 114 c 157 g 215 t 2 others
 ORIGIN

ALIGNMENT SCORES:
 Pred. No.: 8,84e-48 Length: 653
 Score: 473.50 Matches: 90
 Percent Similarity: 88.33% Conservative: 16
 Best Local Similarity: 75.00% Mismatches: 10
 Query Match: 78.01% Indels: 4
 Gaps: 1

US-09-786-715-4 (1-118) x I56999 (1-653)

QY 3 SerSerGIUGLUGLInValIleGIYcYshISserValAspGIUTrPlySGluInPhe 22
 ||||| 69 TCATCCGAGGAGGCAAGTGTTCGCTGCCCAAGAGTTGAGAAATGAGACGACTTC 128
 ||||| 23 GlnIysGIyValAspSerLysLysLeuValAlIleAspPheThrAlaSerTrpCysGly 42
 ||||| 129 AAGAAAGCGTTGAGACTAAGAACTGGTGGTGCATTTTACTGCTTCATGAGTGGCGS 188
 ||||| 43 ProCysArgPheIleAlaProIleuAlaGluMetAlaLysThrProHisValIle 62
 ||||| 189 CCTTGCCTTTATTATGCCCCCAATTCCTGCTGACATGCTTAAGAAAGATGCCCATGTATTA 248
 ||||| QY 63 PheLeuLysValAspValAspGIUleuLysThrValAla-GluGIUphelYsValGIUAl 82
 ||||| Db 249 TTCCTCAAGGTTGATGTGATGAAGTGTTCACGCGGAAATGAGAGTGGAGGC 308
 ||||| QY 82 aMetProThrPheValPheLeuLysGIUGLysGIUValGIUArgLeuValGIYAlaAr 102
 ||||| Db 309 AATGCCAACTTTTCTTCATTAAGAGGAAAGAGTGGCAAGAGTGGTGGCGCA 368
 ||||| QY 102 gLySGluGIUleuGlnAlaThrValGIUlyshISGIYAla-----IleThrAla 118
 |||||

Db 69 TCATCCGAGGAGGCAAGTGTTCGCTGCCCAAGAGTTGAGAAATGAGACGACTTC 128
 QY 23 GlnIysGIyValAspSerLysLysLeuValAlIleAspPheThrAlaSerTrpCysGly 42
 Db 129 AAGAAAGCGTTGAGACTAAGAACTGGTGGTGCATTTTACTGCTTCATGAGTGGCGS 188
 QY 43 ProCysArgPheIleAlaProIleuAlaGluMetAlaLysThrProHisValIle 62
 Db 189 CCTTGCCTTTATTATGCCCCCAATTCCTGCTGACATGCTTAAGAAAGATGCCCATGTATTA 248
 QY 63 PheLeuLysValAspValAspGIUleuLysThrValAla-GluGIUphelYsValGIUAl 82
 Db 249 TTCCTCAAGGTTGATGTGATGAAGTGTTCACGCGGAAATGAGAGTGGAGGC 308
 QY 82 aMetProThrPheValPheLeuLysGIUGLysGIUValGIUArgLeuValGIYAlaAr 102
 Db 309 AATGCCAACTTTTCTTCATTAAGAGGAAAGAGTGGCAAGAGTGGTGGCGCA 368
 QY 102 gLySGluGIUleuGlnAlaThrValGIUlyshISGIYAla-----IleThrAla 118
 Db 369 GAAAGAGAGTTTGCAGCAGACCATATGTAAGACATCTCTCTCTACTGTACTGCT 426

RESULT 10
 159865 LOCUS I59865 Sequence 103 from patent US 5654414.
 159865 DEFINITION I59865
 159865 VERSION I59865.1 GI:2478497
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 653)
 AUTHORS Ryals,J.A., Beck,J.J. and Friedrich,L.B.
 TITL Chemically inducible promoter of a cucumber chitinase/lysozyme gene
 JOURNAL Patent: US 5654414-A 103 05-AUG-1997;
 FEATURES location/Qualifiers
 source 1..653
 BASE COUNT 165 a 114 c 157 g 215 t 2 others
 ORIGIN

ALIGNMENT SCORES:
 Pred. No.: 8,84e-48 Length: 653
 Score: 473.50 Matches: 90
 Percent Similarity: 88.33% Conservative: 16
 Best Local Similarity: 75.00% Mismatches: 10
 Query Match: 78.01% Indels: 4
 Gaps: 1

US-09-786-715-4 (1-118) x I59865 (1-653)

QY 3 SerSerGIUGLUGLInValIleGIYcYshISserValAspGIUTrPlySGluInPhe 22
 ||||| 69 TCATCCGAGGAGGCAAGTGTTCGCTGCCCAAGAGTTGAGAAATGAGACGACTTC 128
 ||||| 23 GlnIysGIyValAspSerLysLysLeuValAlIleAspPheThrAlaSerTrpCysGly 42
 ||||| 129 AAGAAAGCGTTGAGACTAAGAACTGGTGGTGCATTTTACTGCTTCATGAGTGGCGS 188
 ||||| 43 ProCysArgPheIleAlaProIleuAlaGluMetAlaLysThrProHisValIle 62
 ||||| 189 CCTTGCCTTTATTATGCCCCCAATTCCTGCTGACATGCTTAAGAAAGATGCCCATGTATTA 248
 ||||| QY 63 PheLeuLysValAspValAspGIUleuLysThrValAla-GluGIUphelYsValGIUAl 82
 ||||| Db 249 TTCCTCAAGGTTGATGTGATGAAGTGTTCACGCGGAAATGAGAGTGGAGGC 308
 ||||| QY 82 aMetProThrPheValPheLeuLysGIUGLysGIUValGIUArgLeuValGIYAlaAr 102
 ||||| Db 309 AATGCCAACTTTTCTTCATTAAGAGGAAAGAGTGGCAAGAGTGGTGGCGCA 368
 ||||| QY 102 gLySGluGIUleuGlnAlaThrValGIUlyshISGIYAla-----IleThrAla 118
 |||||

QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
 DB 189 CTTGGCCGTTTATGCCCCCAATTCCTTGATGACATGCTAAGAAAGATGCCCATGTTATA 248
 QY 63 PheLeuLysValAspValAspGluLeuLysThrValAla-GluGluPheLysValAla 82
 DB 249 TTCCTCAAGGTGATGTTGATGAACGAGACTGTTTCAGCCGGGAATGGAGTGTGGAGGC 308
 QY 82 ametProThrPheValPheLeuLysGluLysGluValGluArgLeuValGlyAlaAr 102
 DB 309 AATGCCACTTTTGTCTTCATTAAGATGGAAGAAGATGGACAGATGTTGTGCCCA 368
 QY 102 glySGluGluLeuGlnAlaThrValGluLysHisGlyAla-----IleThrAla 118
 DB 369 GAAAGAGAGATTGCACAGACCATAGTGAAGCATGCTGCTCTGCTACTGCTACTGCT 426
 RESULT 6
 AR064647 653 bp DNA linear PAT 29-SEP-1999
 LOCUS AR064647
 DEFINITION Sequence 103 from patent US 5847258.
 ACCESSION AR064647
 VERSION AR064647.1 GI:5993955
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 653)
 AUTHORS Ryals,J.A., Moyer,M.B., Payne,G.B. and Ward,E.R.
 TITLE DNA encoding beta-1,3-glucanases
 JOURNAL Patent: US 5847258-A 103 08-DEC-1998;
 FEATURES
 source 1. 653
 BASE COUNT 165 a 114 c 157 g 215 t 2 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 8.84e-48 Length: 653
 Score: 473.50 Matches: 90
 Percent Similarity: 88.33% Conservative: 16
 Best Local Similarity: 75.00% Mismatches: 10
 Query Match: 78.01% Indels: 4
 DB: 6 Gaps: 1
 US-09-786-715-4 (1-118) x AR064647 (1-653)
 QY 3 SerSerGluGluGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
 DB 69 TCATCCGAGAGGAGGACAAAGTTCGGCTGCCACAAAGTTGAGGAATGAAACGATCACTTC 128
 QY 23 GlnLysGlyValAspSerLysLysLeuValIleAspPheThrAlaSerTrpCysGly 42
 DB 129 AAGAAAGGCGTGGAGACTAAGAAACGCTGGTGGTGGATTTTACTCTTCATGTCGGS 188
 QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
 DB 189 CTTGGCCGTTTATGCCCCCAATTCCTTGATGACATGCTAAGAAAGATGCCCATGTTATA 248
 QY 63 PheLeuLysValAspValAspGluLeuLysThrValAla-GluGluPheLysValAla 82
 DB 249 TTCCTCAAGGTGATGTTGATGAACGAGACTGTTTCAGCCGGGAATGGAGTGTGGAGGC 308
 QY 82 ametProThrPheValPheLeuLysGluLysGluValGluArgLeuValGlyAlaAr 102
 DB 309 AATGCCACTTTTGTCTTCATTAAGATGGAAGAAGATGGACAGATGTTGTGCCCA 368
 QY 102 glySGluGluLeuGlnAlaThrValGluLysHisGlyAla-----IleThrAla 118
 DB 369 GAAAGAGAGATTGCACAGACCATAGTGAAGCATGCTGCTCTGCTACTGCTACTGCT 426
 RESULT 7
 AR067572

LOCUS AR067572 653 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 103 from patent US 5851766.
 ACCESSION AR067572
 VERSION AR067572.1 GI:5998794
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 653)
 AUTHORS Ryals,J.A. and Harms,C.
 TITLE Process for isolating chemically regulatable DNA sequences
 JOURNAL Patent: US 5851766-A 103 22-DEC-1998;
 FEATURES
 source 1. 653
 BASE COUNT 165 a 114 c 157 g 215 t 2 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 8.84e-48 Length: 653
 Score: 473.50 Matches: 90
 Percent Similarity: 88.33% Conservative: 16
 Best Local Similarity: 75.00% Mismatches: 10
 Query Match: 78.01% Indels: 4
 DB: 6 Gaps: 1
 US-09-786-715-4 (1-118) x AR067572 (1-653)
 QY 3 SerSerGluGluGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
 DB 69 TCATCCGAGAGGAGGACAAAGTTCGGCTGCCACAAAGTTGAGGAATGAAACGATCACTTC 128
 QY 23 GlnLysGlyValAspSerLysLysLeuValIleAspPheThrAlaSerTrpCysGly 42
 DB 129 AAGAAAGGCGTGGAGACTAAGAAACGCTGGTGGTGGATTTTACTCTTCATGTCGGS 188
 QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
 DB 189 CTTGGCCGTTTATGCCCCCAATTCCTTGATGACATGCTAAGAAAGATGCCCATGTTATA 248
 QY 63 PheLeuLysValAspValAspGluLeuLysThrValAla-GluGluPheLysValAla 82
 DB 249 TTCCTCAAGGTGATGTTGATGAACGAGACTGTTTCAGCCGGGAATGGAGTGTGGAGGC 308
 QY 82 ametProThrPheValPheLeuLysGluLysGluValGluArgLeuValGlyAlaAr 102
 DB 309 AATGCCACTTTTGTCTTCATTAAGATGGAAGAAGATGGACAGATGTTGTGCCCA 368
 QY 102 glySGluGluLeuGlnAlaThrValGluLysHisGlyAla-----IleThrAla 118
 DB 369 GAAAGAGAGATTGCACAGACCATAGTGAAGCATGCTGCTCTGCTACTGCTACTGCT 426
 RESULT 8
 I38524
 LOCUS I38524 653 bp DNA linear PAT 13-MAY-1997
 DEFINITION Sequence 103 from patent US 5614395.
 ACCESSION I38524
 VERSION I38524.1 GI:2084578
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 653)
 AUTHORS Ryals,J.A., Alexander,D.C., Beck,J.J., Duesing,J.H., Goodman,R.M.,
 Friedrich,L.B., Harms,C., Meins,F. Jr., Montoya,A. deceased,
 Moyer,M.B., Neuhaus,J.-M., Payne,G.B., Sperisen,C., Stinson,J.R.,
 Uknes,S.J., Ward,E.R. and Williams,S.C.
 TITLE Chemically regulatable and anti-pathogenic DNA sequences and uses
 JOURNAL Patent: US 5614395-A 103 25-MAR-1997;
 FEATURES
 source 1. 653
 /organism="unknown"

AR020895	LOCUS	AR020895	653 bp	DNA	linear	PAT 05-DEC-1998
	DEFINITION	Sequence	103	from patent US 5789214.		
	ACCESSION	AR020895				
	VERSION	AR020895.1	GI:3975510			
	KEYWORDS					
	SOURCE	Unknown.				
	ORGANISM	Unknown.				
		Unclassified.				
REFERENCE		1 (bases 1 to 653)				
AUTHORS		Ryals,J.A., Friedrich,L.B., Uknes,S.J. and Ward,E.R.				
TITLE		Method of inducing gene transcription in a plant				
JOURNAL		Patent: US 5789214-A 103 04-ARG-1998;				
FEATURES		Location/Qualifiers				
Source		1..653				
		/organism="unknown"				
BASE COUNT		165 a	114 c	157 g	215 t	2 others
ORIGIN						

Alignment Scores:	
Pred. No.:	8.84e-48
Score:	473.50
Percent Similarity:	88.33%
Best Local Similarity:	75.00%
Query Match:	78.01%
Db:	6
Length:	653
Matches:	90
Conservative:	16
Mismatches:	10
Indels:	1
Gaps:	1

QY 3 serseglugluglvglvalllelglycshsserValaspGltThrpysgluglnp 22
Db 69 TcATCCGAGGAGGCAAGTGTTCGGCTGCCCAAGCTTGACGAATGACAGACTTTC 128
QY 23 GlnysglYValaspSerLysLysLeuValAlIaspPhThAlaserTrpcsgly 42
Db 129 AAGAAAGCGGTGAGACTAGAAACTGGGTGGTGCATTTACTCGTTCATGGTCCGS 188
QY 43 ProCysArpHeIleAlaProIleLeuAlaGluMetAlaLysThrProHIsValIle 62
Db 189 CCTTGCGCTTTATTGGCCCAATCTTGCTGCACATTGCAAGAAAGATGCCCATGTTATA 248
QY 63 PheLeuysValaspValaspGluLeuLysThrValAlaIle-GluGluPheLysValGluAl 82
Db 249 TTCCCAAGGTGTGATGTGATGACATGGAAGACTGTTCACGCCGAATGAGTGTGGAGGC 308
QY 82 ameLeProThrpheValPheLeuLysGluGlyLysGluValGluArgLeuValAlaIaAr 102
Db 309 AATGCACACTTTTGCTTCATTAAAGATGAGAAAGAAAGATGCACAGCTGTGGTGGCCA 368
QY 102 gLysgGluGluLeuGlnAlaThrValGluLysHIsGlyAla-----IleThrAla 118
Db 369 GAAAGAGAGATTGCACGACCAATGAGAAAGCATCTGCTCCGTACTGTGATGCTCT 426

RESULT 4	LOCUS	AR027218	653 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	Sequence 103 from patent US 5856154.					
ACCESSION	AR027218					
VERSION	AR027218.1	GI:5938058				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1 (bases 1 to 653)					
TITLE	Ryals,J.A., Alexander,D.C., Goodman,R.M. and Ward,E.R.					
JOURNAL	Method of protecting plants from oomycete pathogens					
FEATURES	Patent: US 5856154-A 103 05-JAN-1999;					
source	Location/Qualifiers					
	1..653					
	/organism="unknown"					
BASE COUNT	165 a 114 c 157 g 215 t					
ORIGIN						
	2 others					

Alignment Scores:	
Pred. NO.:	8, 84e-48
Score:	473.50
Percent Similarity:	88.33%
Best Local Similarity:	75.00%
Query Match:	78.01%
DB:	6
Length:	653
Matches:	90
Conservative:	16
Mismatches:	10
Indels:	1
Gaps:	1

	US-09-786-715-4 (1-118) x AR027218 (1-653)
QY	3 SerSerGIuGIuGIuValIIeGIyShISerValaSPuITrIPlySGluInphe 22
Db	69 TCATTCGCGAGGGGCAAGATGTTCGGGCCACCAAGGTGGAGATGGAACAGTACTTC 128
QY	23 GlnIysGIyValaSPserLySLysIneuValIIeaSPpHeThaISerTpcSGly 42
Db	129 AAGAAAGCGGTGAGACTAAGAAACTGGGTGGTGCATTTACTGCTTCACATGGGCGGS 188
QY	43 ProCysATpPheIIeaIaProIIeIuValIaGluMeTaIaLySLysThProHISaIIle 62
Db	189 CCTTGCCGCTTTTATTATGCCCAATTCCTCTGCATTCGTAAAGACATGCCCATTTATA 248
QY	63 PheLeuLyValaSPValaSPGIuDeuLySThrValaIa-GluGIuPheLyValaGluAl 82
Db	249 TTTCSCAAGTGTGATGTGATGAACGTGAAGACTGTTCAGGGGGAATGGAGGTGGAGGC 308
QY	82 aMeCpRoThrPheValIPheLeuLySGIuLySGIuValaGIuATrGLeuValaGlyAlaAr 102
Db	309 AATGCACAATTGTGCTTCATTAAAGATGAAGAAAGAAAGTGAACAGATGTTGGTGCCAA 368
QY	102 gLySGIuGIuDeuGlnaIaThrValaGIuLySInISGlyLa-----IIeThaIa 118
Db	369 GAAAGAGAGATTGCAGCAGACCAATAGTAACATATCTGCTCTACTGACACTGCT 426

LOCUS	AR038505	653 bp	DNA	linear	PAT 29-SEP-1999
DEFINITION	Sequence 103 from patent US 5804693.				
ACCESSION	AR038505				
VERSION	AR038505.1				
KEYWORDS	GI:5957222				
SOURCE	unknown.				
ORGANISM	unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 653)				
	Gaffney,T.D., Ryals,J.A., Friedrich,L.B., Uknes,S.J., Ward,E.R.,				
	Kessmann,H. and Vernoolt,J.B.T.				
TITLE	Chemically regulatable and anti-pathogenic DNA sequences and uses thereof				
JOURNAL	Patent: US 5804693-A 103 08-SEP-1998;				
FEATURES	Location/Qualifiers				
source	1..653				
	/organism="unknown"				
BASE COUNT	165 a 114 c 157 g 215 t				
ORIGIN					
Alignment Scores:					
Pred. No.:	8.84e-48	Length:	653		
Score:	473.50	Matches:	90		
Percent Similarity:	88.33%	Conservative:	16		
Best Local Similarity:	75.00%	Mismatches:	10		
Query Match:	78.01%	Indels:	4		
DB:	6	Gaps:	1		
US-09-786-715-4 (1-118) x AR038505 (1-653)					
OY	3 SerSergIugIugIyglInValIleGlYcYshISserValaSpGIuTrPlySgluGInPhe	22			
Db	69 TCATCCGAGGAGGACAAAGTGTTCGGCGCCACAAAGGTTGAGGAATGGAACGAGTACTTC	128			
OY	23 GlnYsgIyValaSpSerIySlySlyLeuValValIleAspIheTrpIcysGly	42			
Db	129 AAGGAAGCGCTTGAGACTAAGAAACTGGTGGTGCATTTTACTGCTTCATGGTGGCGS	188			

Db 298 ATGCCAACTTTATTTCTTAAGAGTGAAGAAATAGTGACAAACTGTGGTCGGAT 357
 QY 101 LysValGlyLeu 104
 Db 358 AAAGATGGCTG 369
 RESULT 7
 B0888094
 LOCUS B0888094
 DEFINITION P003F02 Populus petioles cDNA library Populus tremula cDNA 5 prime,
 mRNA sequence.
 ACCESSION B0888094
 VERSION B0888094.1 GI:24099159
 KEYWORDS EST.
 SOURCE Populus tremula
 ORGANISM Populus tremula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Malpighiales; Salicaceae; Populus.
 REFERENCE 1 (bases 1 to 612)
 AUTHORS Uneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries
 JOURNAL Unpublished
 COMMENT Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 FEATURES
 source 1..612
 /organism="Populus tremula"
 /mol_type="mRNA"
 /db_xref="taxon:113636"
 /tissue_type="petioles"
 /clone_lib="Populus petioles cDNA library"
 BASE COUNT 161 a 97 c 160 g 194 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3,59e-39 Length: 612
 Score: 385.00 Matches: 70
 Percent Similarity: 78.85% Conservative: 12
 Best Local Similarity: 67.31% Mismatches: 22
 Query Match: 60.44% Indels: 0
 Gaps: 0
 DB: 13
 US-09-786-715-2 (1-122) x B0888094 (1-612)
 QY 1 MetlaGluGluGlyGlnValIleAlaCysHisLysIleAspGluTrpGluGlyGlnLeu 20
 Db 56 ATGGCCGAGAGGACAGATTATGCTCCGACACAGTGTACCTGGAAGAGCATTTTC 115
 QY 21 GlyLysTrpLysAspSerGluLysLeuValValAlaAspPheThrAlaSerTrpCysGly 40
 Db 116 GAGAAAGGAAAGGGCTCAGAAACTGATTCGCGATTTTACTGCTTCATGGGTCCA 175
 QY 41 ProCysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnProAsnValAla 60
 Db 176 CCATGTAAATGATGCTCCCAATCTCCGCGATGGCAGAGGATTCCTAATGTCCA 235
 QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
 Db 236 TTCTTGAAGGTGATGATGAATGAAGCTGTCTGAGAGTGAATGTGGAGGCA 295
 QY 81 MetProThrPheValPheLeuLysGlyLysIleIleGluLysIleValGlyAlaAsp 100
 Db 296 ATGCCAACTTTATTTCTTGAAGATGGAATAATTAGTGACAAACTGTGGTCTGAT 355
 QY 101 LysValGlyLeu 104
 ||| |||||

Db 356 AAAGATGGCTG 367
 RESULT 8
 B0830685
 LOCUS B0830685
 DEFINITION T011F03 Populus apical shoot cDNA library Populus tremula x Populus
 tremuloides cDNA 5 prime, mRNA sequence.
 ACCESSION B0830685
 VERSION B0830685.1 GI:24008183
 KEYWORDS EST.
 SOURCE Populus tremula x Populus tremuloides
 ORGANISM Populus tremula x Populus tremuloides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Malpighiales; Salicaceae; Populus.
 REFERENCE 1 (bases 1 to 615)
 AUTHORS Uneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries
 JOURNAL Unpublished
 COMMENT Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 FEATURES
 source 1..615
 /organism="Populus tremula x Populus tremuloides"
 /mol_type="mRNA"
 /db_xref="taxon:47664"
 /tissue_type="apical shoot"
 /clone_lib="Populus apical shoot cDNA library"
 BASE COUNT 154 a 97 c 161 g 203 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3,61e-39 Length: 615
 Score: 385.00 Matches: 70
 Percent Similarity: 78.85% Conservative: 12
 Best Local Similarity: 67.31% Mismatches: 22
 Query Match: 60.44% Indels: 0
 Gaps: 0
 DB: 13
 US-09-786-715-2 (1-122) x B0830685 (1-615)
 QY 1 MetlaGluGluGlyGlnValIleAlaCysHisLysIleAspGluTrpGluGlyGlnLeu 20
 Db 35 ATGGCCGAGAGGACAGATTATGCTCCGACACAGTGTACCTGGAAGAGCATTTTC 94
 QY 21 GlyLysTrpLysAspSerGluLysLeuValValAlaAspPheThrAlaSerTrpCysGly 40
 Db 95 GAGAAAGGAAAGGGCTCAGAAACTGATTCGCGATTTTACTGCTTCATGGGTCCA 154
 QY 41 ProCysArgAlaIleAlaProTyrPheThrGluLeuAlaLysAsnProAsnValAla 60
 Db 155 CCATGTAAATGATGCTCCCAATCTCCGCGATGGCAGAGGATTCCTAATGTCCA 214
 QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
 Db 215 TTCTTGAAGGTGATGATGAATGAAGCTGTCTGAGAGTGAATGTGGAGGCA 274
 QY 81 MetProThrPheValPheLeuLysGlyLysIleIleGluLysIleValGlyAlaAsp 100
 Db 275 ATGCCAACTTTATTTCTTGAAGATGGAATAATTAGTGACAAACTGTGGTCTGAT 334
 QY 101 LysValGlyLeu 104
 ||| |||||

RESULT 9
 B0873533

LOCUS B0873533 641 bp mRNA linear EST 16-OCT-2002
 DEFINITION 0056f01 Populus flower cDNA library Populus balsamifera subsp.
 trichocarpa cDNA 5 prime, mRNA sequence.
 ACCESSION B0873533
 VERSION B0873533.1 GI:24065057
 KEYWORDS EST.
 SOURCE Populus balsamifera subsp. trichocarpa
 ORGANISM Populus balsamifera subsp. trichocarpa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eucosids I; Malpighiales; Salicaceae; Populus.
 REFERENCE 1 (bases 1 to 641)
 AUTHORS Uneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries
 JOURNAL Unpublished
 COMMENT Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 FEATURES
 source location/Qualifiers
 1..641
 /organism="Populus balsamifera subsp. trichocarpa"
 /mol_type="mRNA"
 /sub_species="trichocarpa"
 /db_xref="taxon:3694"
 /clone_lib="Populus flower cDNA library"
 /note="Organ: flower"
 BASE COUNT 163 a 102 c 175 g 201 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 3,82e-39 Length: 641
 Score: 385.00 Matches: 70
 Percent Similarity: 78.85% Conservative: 12
 Best Local Similarity: 67.31% Mismatches: 22
 Query Match: 60.44% Indels: 0
 DB: 13 Gaps: 0
 US-09-786-715-2 (1-122) x B0873533 (1-641)
 QY 1 MetAlaGlUGlUGlInValIleAlaCySHsLysIleAspGluTrpGluGlnLeu 20
 Db 86 ATGGCGGAGAAAGCAAGTATTCGCGCACACAGTGATACCTGGAAAGCAATTTC 145
 QY 21 GtLyStRpLysAspSerGluLysLeuValValAlaSpPheThrAlaSerTrpCysGly 40
 Db 146 GAGAAAGGAAAGCGGCTCGAAGAACTGATGTCGTGATTTACTGCTTCATGTCCTCA 205
 QY 41 ProCyArGAlaIleAlaProTyRphThrGluLeuAlaLysAsnSnpProAsnValAla 60
 Db 206 CCATGTAAATGATTCCTCCATCTTCGCCGAGAGTGGCGAAGATTTCCTAATGTGCACA 265
 QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
 Db 266 TTCTTGAAGGTGATGTGATGAATGAAGCGCTGTTGCGAGAGTGAATGTGAGCGCA 325
 QY 81 MetProThrPheValPheLeuLysGlyLysIleIleGluLysIleValGlyAlaAsp 100
 Db 326 ATGCCCAACTTTATTTCTCGAAGAAATGAGAAATTAAGTGACAAACTGTGGTGCTGAT 385
 QY 101 LysValGlyLeu 104
 Db 386 AAAAGATGGCCTG 397
 RESULT 10
 LOCUS B0885783 520 bp mRNA linear EST 17-OCT-2002
 DEFINITION R036A12 Populus root cDNA library Populus tremula x Populus
 tremuloides cDNA 5 prime, mRNA sequence.

ACCESSION B0885783
 VERSION B0885783.1 GI:24077300
 KEYWORDS EST.
 SOURCE Populus tremula x Populus tremuloides
 ORGANISM Populus tremula x Populus tremuloides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eucosids I; Malpighiales; Salicaceae; Populus.
 REFERENCE 1 (bases 1 to 520)
 AUTHORS Uneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries
 JOURNAL Unpublished
 COMMENT Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 FEATURES
 source location/Qualifiers
 1..520
 /organism="Populus tremula x Populus tremuloides"
 /mol_type="mRNA"
 /db_xref="taxon:47664"
 /tissue_type="root"
 /clone_lib="Populus root cDNA library"
 BASE COUNT 131 a 89 c 138 g 162 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.21e-39 Length: 520
 Score: 383.00 Matches: 70
 Percent Similarity: 80.77% Conservative: 14
 Best Local Similarity: 67.31% Mismatches: 20
 Query Match: 60.13% Indels: 0
 DB: 13 Gaps: 0
 US-09-786-715-2 (1-122) x B0885783 (1-520)
 QY 1 MetAlaGlUGlUGlInValIleAlaCySHsLysIleAspGluTrpGluGlnLeu 20
 Db 27 ATGGCAGAAAGAAAGCAAGTATTCGCGCACACCGTGTGATGTCGGAAAGCAATTTC 86
 QY 21 GtLyStRpLysAspSerGluLysLeuValValAlaSpPheThrAlaSerTrpCysGly 40
 Db 87 GAGAAAGGAAAGGAGCTCGAAGCTGATGTGTCGTGATTTACTGCTTCATGTCCTCCT 146
 QY 41 ProCyArGAlaIleAlaProTyRphThrGluLeuAlaLysAsnSnpProAsnValAla 60
 Db 147 CCATGTAAATGATTCCTCCGCAATTTCCGCGATTTGGCCAAAGATTCCACCAATGTCCACC 206
 QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
 Db 207 TTCTTGAAGGTGATGTGATGAATGAAGCGCTGTTGCGGAGTGAAGTGCAGGCG 266
 QY 81 MetProThrPheValPheLeuLysGlyLysIleIleGluLysIleValGlyAlaAsp 100
 Db 267 ATGCCCAACTTTATTTCTCGAAGAAAGCAAGAAATTAAGTGACAAATTTGTGGTGCTGAT 326
 QY 101 LysValGlyLeu 104
 Db 327 AAAAGATGGCCTC 338
 RESULT 11
 LOCUS B0812532 523 bp mRNA linear EST 15-OCT-2002
 DEFINITION UL97TE03 Populus leaf cDNA library Populus tremula x Populus
 tremuloides cDNA 5 prime, mRNA sequence.
 ACCESSION B0812532
 VERSION B0812532.1 GI:23967453
 KEYWORDS EST.
 SOURCE Populus tremula x Populus tremuloides

ORGANISM *Populus tremula* x *Populus tremuloides*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Malpighiales; Salicaceae; *Populus*.

REFERENCE 1 (bases 1 to 523)
 Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
 The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries

JOURNAL Unpublished
 COMMENT Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 Location/Qualifiers

FEATURES
 source 1..523
 /organism="Populus tremula x Populus tremuloides"
 /mol_type="mRNA"
 /db_xref="taxon:47664"
 /clone_lib="Populus leaf cDNA library"
 /note="Organ: leaf"

BASE COUNT 141 a 93 c 140 g 149 t

ORIGIN

Alignment Scores:
 Pred. No.: 5,25e-39 Length: 523
 Score: 383.00 Matches: 70
 Percent Similarity: 80.77% Conservative: 14
 Best Local Similarity: 67.31% Mismatches: 20
 Query Match: 60.13% Indels: 0
 DB: 13 Gaps: 0

US-09-786-715-2 (1-122) x B0812532 (1-523)

QY 1 Metatagluglglglnvalillealacyshtslsyleaspclutripcluglgnleu 20
 |||||
 DB 74 ATGCAGAGAAGAGACAGTGTGCTCCGCCACCGCTGTCTGGAAAGACAATTC 133
 |||||

QY 21 GlylstrplysAspSerclulysleuvalvalialaspPheThAlaserTrpCysgly 40
 |||||
 DB 134 GAGAAGGAGAAAGGAGCTCAGACGCTGATGTGGTGATTTTACTGCTTCATGCTGCTCT 193
 |||||

QY 41 ProcysatgAlaIleAlaProtyrPheThrgluleuAlaIalysAsnAsnProAsnValAla 60
 |||||
 DB 194 CCATGTAATTCATTCATTCGCCCAATTTTCGGCGATTTGGCCAGACAAGTTTACCAATGTCACC 253
 |||||

QY 61 PheleulysValaspValaspcluleuAsnSerValAlaIaserLysTrpGlutlleAsnAla 80
 |||||
 DB 254 TTCTTGAGAGGTGACGTGATGATTAATTAAGACCTGTGCTCGCGACTGGGAATGCGAGCGC 313
 |||||

QY 81 MetProthPheValPheleulysLysglLyslleIleGlulyslleValglYAlaasp 100
 |||||
 DB 314 ATGCCAATCTTTATTTCTCTGAAGACGGAATAATTAAGTGAACAATAATGCTGCTGAT 373
 |||||

QY 101 LysValglYleu 104
 |||||

DB 374 AAAGATGGCCTC 385

RESULT 12
 B0829684 523 bp mRNA linear EST 15-OCT-2002
 LOCUS B0829684
 DEFINITION *Populus apical* shoot cDNA library *Populus tremula* x
Populus tremuloides cDNA 5 prime, mRNA sequence.
 ACCESSION B0829684
 VERSION B0829684.1 GI:24005929
 KEYWORDS EST.
 SOURCE *Populus tremula* x *Populus tremuloides*
 ORGANISM *Populus tremula* x *Populus tremuloides*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Malpighiales; Salicaceae; *Populus*.

REFERENCE 1 (bases 1 to 523)
 Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
 The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries

JOURNAL Unpublished
 COMMENT Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 Location/Qualifiers

FEATURES
 source 1..523
 /organism="Populus tremula x Populus tremuloides"
 /mol_type="mRNA"
 /db_xref="taxon:47664"
 /tissue_type="apical shoot"
 /clone_lib="Populus apical shoot cDNA library"

BASE COUNT 138 a 92 c 138 g 155 t

ORIGIN

Alignment Scores:
 Pred. No.: 5,25e-39 Length: 523
 Score: 383.00 Matches: 70
 Percent Similarity: 80.77% Conservative: 14
 Best Local Similarity: 67.31% Mismatches: 20
 Query Match: 60.13% Indels: 0
 DB: 13 Gaps: 0

US-09-786-715-2 (1-122) x B0829684 (1-523)

QY 1 Metatagluglglglnvalillealacyshtslsyleaspclutripcluglgnleu 20
 |||||
 DB 59 ATGCAGAGAAGAGACAGTGTGCTCCGCCACCGCTGTCTGGAAAGACAATTC 118
 |||||

QY 21 GlylstrplysAspSerclulysleuvalvalialaspPheThAlaserTrpCysgly 40
 |||||
 DB 119 GAGAAGGAGAAAGGAGCTCAGACGCTGATGTGGTGATTTTACTGCTTCATGCTGCTCT 178
 |||||

QY 41 ProcysatgAlaIleAlaProtyrPheThrgluleuAlaIalysAsnAsnProAsnValAla 60
 |||||
 DB 179 CCATGTAATTCATTCATTCGCCCAATTTTCGGCGATTTGGCCAGACAAGTTTACCAATGTCACC 238
 |||||

QY 61 PheleulysValaspValaspcluleuAsnSerValAlaIaserLysTrpGlutlleAsnAla 80
 |||||
 DB 238 TTCTTGAGAGGTGACGTGATGATTAATTAAGACCTGTGCTCGCGAGTGGAGAGTGCAGCGC 298
 |||||

QY 81 MetProthPheValPheleulysLysglLyslleIleGlulyslleValglYAlaasp 100
 |||||
 DB 299 ATGCCAATCTTTATTTCTCTGAAGACGGAATAATTAAGTGAACAATAATGCTGCTGAT 358
 |||||

QY 101 LysValglYleu 104
 |||||

DB 359 AAAGATGGCCTC 370

RESULT 13
 B1136756 531 bp mRNA linear EST 31-DEC-2001
 LOCUS B1136756
 DEFINITION *Populus flower* cDNA library *Populus balsamifera* subsp.
trichocarpa cDNA, mRNA sequence.
 ACCESSION B1136756
 VERSION B1136756.1 GI:18017704
 KEYWORDS EST.
 SOURCE *Populus balsamifera* subsp. *trichocarpa*
 ORGANISM *Populus balsamifera* subsp. *trichocarpa*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Malpighiales; Salicaceae; *Populus*.

REFERENCE 1 (bases 1 to 531)
 Hertzberg, M., Aspeborg, H., Erlandsson, R., Björkbacka, H., Hiltunen
 T., Karlsson, J., Teeri, T., Gustafsson, P., Bhalerao, R., Jansson, S.,
 Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M., Sandberg, C. and

TITLE Lundeberg, U.
JOURNAL Gene expression in Populus
COMMENT Unpublished
Contact: Eriandsson R
Department of Biotechnology
Royal Institute of Technology
Teknikringen 30, Stockholm S-10044, Sweden
Tel: 46 8 790 8287
Fax: 46 8 245452
Email: riker1@biochem.kth.se.

FEATURES
source
1..531
/organism="Populus balsamifera subsp. trichocarpa"
/mol_type="mRNA"
/sub_species="trichocarpa"
/db_xref="taxon:3694"
/clone_lib="Populus flower cDNA library"
/note="organ: flower"

BASE COUNT 140 a 84 c 147 g 160 t
ORIGIN

Alignment Scores:
Pred. No.: 5,36e-39 Length: 531
Score: 383.00 Matches: 70
Percent Similarity: 80.77% Conservative: 14
Best Local Similarity: 67.31% Mismatches: 20
Query Match: 60.13% Indels: 0
DB: 12 Gaps: 0

US-09-786-715-2 (1-122) x B1136756 (1-531)

QY 1 MetAlaGlUGlUGlGlnValIleAlaCySHsLysIleAspGluTrpGluGlnLeu 20
|||||
Db 52 ATGGCAGAGAAAGAGACAGATGATGCGTCGCCACACCGATGCTGGAAGAGCAATTC 111
|||||

QY 21 GtLYSTrPLysAspSerGluLysLeuValValAlaSpPheThrAlaSerTrpGly 40
|||||
Db 112 GAGAGGGAAGAGGAGCTGAGAGCTGATGCTGATTTACTCTCATGCTCCCT 171
|||||

QY 41 ProCyARgAlAlleAlaProTyrrPheThrGluLeuAlaLysAsnProAsnValAla 60
|||||
Db 172 CCATGTAATTCATTCGCGCAGTTTCGGGATTTGGCCAGAAAGTCAACCATGTCACC 231
|||||

QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
|||||
Db 232 TTCCTTAAGGTGACCTGATGTAATGAAGCCCTGTCGCGAGTGGAGAGCGCG 291
|||||

QY 81 MetProThrPheValPheLeuLysLysIleIleGluLysIleValGlyAlaasp 100
|||||
Db 292 ATGCCAAGCTTTATTTCTCGTAAGATGGAAATTAAGTGACAAATGTGGGTCTGAT 351
|||||

QY 101 LysValGlyLeu 104
|||
Db 352 AAGATGGCCTC 363
|||

RESULT 14
B0884977 532 bp mRNA linear EST 17-OCT-2002
LOCUS B0884977
DEFINITION R018H02 Populus root cDNA library Populus tremula x Populus
tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION B0884977
VERSION B0884977.1 GI:24076494
KEYWORDS
SOURCE
ORGANISM
Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE
AUTHORS
TITLE
JOURNAL
Lundeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished

COMMENT Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
source
1..532
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue_type="root"
/clone_lib="Populus root cDNA library"

BASE COUNT 139 a 90 c 141 g 162 t
ORIGIN

Alignment Scores:
Pred. No.: 5,37e-39 Length: 532
Score: 383.00 Matches: 70
Percent Similarity: 80.77% Conservative: 14
Best Local Similarity: 67.31% Mismatches: 20
Query Match: 60.13% Indels: 0
DB: 13 Gaps: 0

US-09-786-715-2 (1-122) x B0884977 (1-532)

QY 1 MetAlaGlUGlUGlGlnValIleAlaCySHsLysIleAspGluTrpGluGlnLeu 20
|||||
Db 43 ATGGCAGAGAAAGAGACAGATGATGCGTCGCCACACCGTGTGATTCGGAAGAGCAATTC 102
|||||

QY 21 GtLYSTrPLysAspSerGluLysLeuValValAlaSpPheThrAlaSerTrpGly 40
|||||
Db 103 GAGAGGGAAGAGGAGCTGAGAGCTGATGCTGATTTACTCTCATGCTCCCT 162
|||||

QY 41 ProCyARgAlAlleAlaProTyrrPheThrGluLeuAlaLysAsnProAsnValAla 60
|||||
Db 163 CCATGTAATTCATTCGCGCAGTTTCGGGATTTGGCCAGAAAGTTCACCAATGTCACC 222
|||||

QY 61 PheLeuLysValAspValAspGluLeuAsnSerValAlaSerLysTrpGluIleAsnAla 80
|||||
Db 223 TTCCTTAAGGTGACCTGATGTAATGAAGCCCTGTCGCGAGTGGAGAGCGCG 282
|||||

QY 81 MetProThrPheValPheLeuLysLysIleIleGluLysIleValGlyAlaasp 100
|||||
Db 283 ATGCCAAGCTTTATTTCTCGTAAGAGAGCAAAATTAAGTGACAAATGTGGGTCTGAT 342
|||||

QY 101 LysValGlyLeu 104
|||
Db 343 AAGATGGCCTC 354
|||

RESULT 15
B0827985 544 bp mRNA linear EST 15-OCT-2002
LOCUS B0827985
DEFINITION K014P03P Populus apical shoot cDNA library Populus tremula x
Populus tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION B0827985
VERSION B0827985.1 GI:24002337
KEYWORDS
SOURCE
ORGANISM
Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE
AUTHORS
TITLE
JOURNAL
Lundeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished
Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 17:46:53 ; Search time 165.884 Seconds

(without alignments)
1920.219 Million cell updates/sec

Title: US-09-786-715-4

Perfect score: 607

Sequence: 1 MASSEGVIGCHSDVEMKE.....VGARKEELQATVEKHGATTA 118

Scoring table:
BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=rlp
-O=cgna_1/USPTO.spool/US09786715/runat_11082003_150513_6025/app_query.fasta_1.1052
-DB=N_Geneseq_19jun03 -QEMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum2 -TRANS=human40.cdl
-LIST=45 -DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAULEN=2000000000
-USER=US09786715.GCGN_1.1_874_Enunat_11082003_150513_6025 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESUBSTRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_19jun03:*

1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	607	100.0	574	21	AAZ51738
2	473.5	78.0	653	16	AAQ98783
3	473.5	78.0	653	20	AAV62799
4	473.5	78.0	653	20	AAV81683
5	446	73.5	601	21	AAZ51740
6	437	72.0	392	25	ABX18045
7	434	71.5	402	25	ABX21664
8	433.5	71.4	509	22	AAH87768
9	430	70.8	390	25	ABX19403
10	430	70.8	738	21	AAZ51739
11	421	69.4	419	21	AAA31942
12	420	69.2	3888	24	ABSS3097
13	420	69.2	3888	24	ABN89581
14	419	69.0	345	24	ABZ12358
15	419	69.0	345	24	ABN89587
16	419	69.0	470	21	AAC37781
17	419	69.0	561	21	AAC51522
18	419	69.0	563	21	AAC34121
19	419	69.0	3129	24	ABSS3095
20	419	69.0	3129	24	ABN89579
21	419	69.0	3888	24	ABSS3096
22	419	69.0	3888	24	ABN89580
23	414	68.2	4935	24	ABN89586
24	401	66.1	614	21	AAZ51741
25	392	64.6	560	21	AAC41961
26	391	64.4	524	21	AAC33829
27	390	64.3	686	15	AAQ78205
28	390	64.3	687	21	AAC66375
29	389	64.1	357	24	ABZ13931
30	389	64.1	480	21	AAC36542
31	389	64.1	563	21	AAC34211
32	389	64.1	652	21	AAAC48656
33	388	63.9	353	21	AAA31118
34	386	63.6	328	21	AAA31222
35	382	62.9	572	21	AAAC5209
36	377	62.1	576	25	ABX56868
37	374.5	61.7	360	24	ABZ12359
38	374	61.6	328	21	AAA31097
39	373	61.4	285	21	AAA31225
40	369	60.8	647	21	AAC38520
41	368.5	60.7	590	21	AAC38792
42	368	60.6	346	21	AAA31096
43	367	60.5	297	21	AAA31940
44	364	60.0	320	21	AAA31785
45	362	59.6	341	21	AAA31924

ALIGNMENTS

RESULT 1	AAZ51738
ID	AAZ51738 standard; cDNA; 574 BP.
XX	AAZ51738;
XX	
DT	04-JUL-2000 (first entry)
XX	
DE	Catalpa speciosa thioredoxin cDNA.
XX	
KW	Catalpa speciosa thioredoxin; clone ncs.pk0010.e3; chimeric gene;
KW	transgenic plant; seed storage protein; allergenicity; ss.
XX	
OS	Catalpa speciosa.
XX	
Key	Location/Qualifiers
FT	CDS 63..419

```
FT FT /*tag= a
XX XX /product= "Thioredoxin"
PN MO200014239-A2.
XX 16-MAR-2000.
XX
XX 07-SEP-1999; 99WO-US20420.
XX
XX 08-SEP-1998; 98US-0099501.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX
XX Allen SM, Thorpe CJ, Lu AL;
XX
XX WPI; 2000-256987/22.
XX
XX P-PSDB; AAY70480.
XX
XX New isolated polynucleotide encoding thioredoxin polypeptide is useful
XX for producing transgenic plants with an altered level of thioredoxin -
XX
XX Claim 3; Page 29; 33pp; English.
XX
XX The present cDNA sequence encodes Catalpa speciosa thioredoxin
XX protein. The cDNA was derived from clone ncs-PK010.e3, which was
XX isolated from a cDNA library prepared from C. speciosa developing seed
XX tissue. Chimeric genes encoding all or a portion of the thioredoxin
XX protein, in sense or antisense orientation are constructed, wherein
XX expression of the chimeric gene results in production of altered levels
XX of the thioredoxin protein in a transformed host cell. Thioredoxin is
XX involved in the disassembly of seed storage proteins during germination
XX by reducing S-S bonds and in the bread making process. Over expression of
XX thioredoxin in cereals may reduce the allergenicity of any transgenic
XX protein engineered into cereal crops with high sulfhydryl content.
XX
XX Seq Sequence 574 BP; 171 A; 91 C; 157 G; 155 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 6.3e-71 Length: 574
XX Score: 607.00 Matches: 118
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 21 Gaps: 0
XX
XX US-09-786-715-4 (1-118) x AA251738 (1-574)
XX
XX QY 1 MetAlaSerSerGluGluGluGluValIleGlyCysHisSerValAspGluTrpGlu 20
XX |||||||
XX DB 63 ATGGCTTCTTCAGAAAGAGGACAAAGTATCGGTGGCCACTCCCTCGACGAGTGGAAAGAG 122
XX
XX QY 21 GlnPheGlnLysGlyValAlaSerSerLysLysLeuValValIleAspPheThrAlaSerTrp 40
XX |||||||
XX DB 123 CAGTTCAGAAAGGCTTGACTACTAGAAACTGCTGTAATAGACTTCACGGCTTCTCTG 182
XX
XX QY 41 CysGlyProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHis 60
XX |||||||
XX DB 183 TCGGACATCGCATCGCTTTCATTCGCTCAATCTTGCGATGCGCAAGAACACACCCCAT 242
XX
XX QY 61 ValIlePheLeuLysValAlaAspValAspGluLeuLysThrValAlaGluGluPheLysVal 80
XX |||||||
XX DB 243 GTCATATTCCTGAAATCGACGCGATGAGTCAACAGCTGCTGAGGAAATTCCAAGTG 302
XX
XX QY 81 GlnAlaMetProThrPheValPheLeuLysGluGlyLysGluValAlaGluArgLeuValGly 100
XX |||||||
XX DB 303 GAGGCGATCGCAGACCTTCTGTCTTCCTCAAGAAAGGAAAGAAAGGCTTGTGGGA 362
XX
XX QY 101 AlaArgLysGluGluLeuGlnAlaThrValGluLysHisGlyAlaIleThrAla 118
XX |||||||
XX DB 363 GCAAGGAAGGAGCAATTCGAGGCAACAGTTGAGAAACATCGGCGTACTGTGT 416
XX
XX RESULT 2
XX AA099783
```

```
ID ID AA099783 standard; DNA: 653 BP.
XX XX
XX XX AA099783;
AC AC
XX XX
XX XX 24-JUN-1996 (first entry)
DT DT
XX XX
XX XX Plant SAR gene pl.4.3.
DE DE
XX XX
XX XX SAR; tobacco: protein-synthesis independent gene; cyclohexamide;
XX KM systemic acquired resistance response; pl.4.3; anti-pathogen;
XX KM plant protection; ss.
XX
XX Nicotiana acuminata.
XX
XX WO9519443-A2.
XX
XX 20-JUL-1995.
XX
XX 03-JAN-1995; 95WO-IB00002.
XX
XX 13-JAN-1994; 94US-0181271.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX Alexander DC, Ryals JA, Uknes SJ, Ward ER;
XX
XX WPI; 1995-263872/34.
XX
XX New DNA contg. plant systemic acquired resistance genes - and
XX transgenic plants contg. them, impart disease and pest resistance,
XX also Atradiopsis gene promoter to control DNA transcription
XX
XX Disclosure; Page 61; 85pp; English.
XX
XX This sequence represents the DNA sequence of a tobacco protein-synthesis
XX independent gene. The gene is involved in the regulation of the
XX systemic acquired resistance (SAR) response. This gene is designated
XX pl.4.3. This sequence and AA099784 represent SAR genes that are not used
XX in the recombinant/chimaeric DNA molecules of the invention.
XX
XX AA099784-099790 and AA099806 are SAR genes used in the
XX recombinant/chimaeric DNA molecules of the invention. The wild type
XX genes corresponding to these sequences can all be chemically induced in a
XX plant in a protein-synthesis independent manner. SAR genes are involved
XX in the protection of plants against pests and disease. These sequences
XX were isolated by differential screening of a cDNA library, followed by
XX analysis by Northern hybridisation to RNA in the presence and absence of
XX cyclohexamide. The genes are used in the creation of transgenic plants.
XX Transgenic expression of 2 or more of the recombinant molecules of the
XX invention that encode anti-pathogenic proteins provides a synergistic
XX increase in plant protection, and may also offer protection against a
XX wider range of pathogens.
XX
XX Seq Sequence 653 BP; 165 A; 114 C; 157 G; 215 T; 2 other;
XX
XX Alignment Scores:
XX Pred. No.: 3.73e-53 Length: 653
XX Score: 473.50 Matches: 90
XX Percent Similarity: 88.33% Conservative: 16
XX Best Local Similarity: 75.00% Mismatches: 10
XX Query Match: 78.01% Indels: 4
XX DB: 16 Gaps: 1
XX
XX US-09-786-715-4 (1-118) x AA099783 (1-653)
XX
XX QY 3 SerSerGluGluGluGluValIleGlyCysHisSerValAspGluTrpGluGlnPhe 22
XX |||||||
XX DB 69 TCATTCGAGAGGAGGAAAGTGTTCGCTCCACAAAGTTGAGGAAAGCAAGTACTTC 128
XX
XX QY 23 GlnLysGlyValAlaSerSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
XX |||||||
XX DB 129 AAGAAAGGCGCTTGAGACTAAGAAACTGCTGCTGCTGCTTACTCTTCATGCTCGGS 188
XX
XX QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
```



```

Db      |||||
189 CCTGCCGTTTATGCCCCCAATCTGCTGACATTGCTAAGACAGTGGCCCATGTTATA 248
Qy      63 PheleulsValAspValAspGluLeuLysThrValAlaA-GluGluPheLysValGluAl 82
Db      249 TTCTCCAAAGGTTGATGTTGATGACACTGTTTCAGCGGCAATGAGTGGAGGCG 308
Qy      82 aMeProThrPheValPheLeuLysGluGlyLysGluValGluATGLeuValGlyAlaAr 102
Db      309 AATGCCAATTGTTGCTTCATTAAAGATGGAAGAGAGAGTGGACAGAGTGTGGGCCAA 368
Qy      102 gLysGluGluLeuGlnAlaThrValGluLysHisGlyAlaA-----lIeThrAla 118
Db      369 GAAAGAGGAGTTGCAGCAGACCATATGTAAGACATGCTGCTGCTACTGTCATGCT 426

RESULT 3
AAV62799 standard; cDNA; 653 BP.
XX
AC      AAV62799;
XX
DT      05-MAR-1999 (first entry)
XX
DE      Tobacco SAR CHX independent gene clone 1.4.3.
XX
KW      Chemically regulatable DNA promoter; expression control; pesticide;
KM      herbicide tolerance; systemic acquired resistance gene; ss.
XX
OS      Nicotiana acuminata.
XX
PN      US5851766-A.
XX
PD      22-DEC-1998.
XX
PF      31-MAY-1995; 95US-0456262.
XX
PR      31-MAY-1995; 95US-0456262.
XX
PA      (NOVS ) NOVARTIS FINANCE CORP.
XX
PI      Harms C, Ryals JA;
XX
DR      WPI; 1999-08036/07.
XX
PT      Isolating chemically regulatable DNA sequences in plants - useful
PR      for chemically controlling expression in transformed plants
XX
PS      Example 40A; Column 257-260; 175pp; English.
XX
CC      This sequence represents a clone of the tobacco systemic acquired
CC      resistance (SAR) cyclohexamide (CHX) independent.
CC      This gene can be isolated using the method of the invention.
CC      The method is for isolating a chemically regulatable DNA promoter
CC      fragment from the 5' flanking region of a chemically regulatable gene in
CC      a plant tissue. The method allows isolation of sequences which will be
CC      useful for the controlled expression of genes, under the control of a
CC      non-coding regulatable sequence. This is useful in plants with a
CC      herbicide or pesticide detoxification mechanism under the control of a
CC      chemical regulator, the regulator being applied before or with the
CC      herbicide or pesticide to give optimal tolerance. The promoter fragment
CC      is useful for controlling sequences which encode traits such as
CC      height, shape, development, male or female sterility, and the ability
CC      of the plant to withstand cold, heat, salt and drought. The chemical
CC      induction of the promoter allows the regulation of production of
CC      compounds, e.g. flavours, fragrances, pigments, natural sweeteners,
CC      industrial feedstocks, antimicrobials and pharmaceuticals, by
CC      biosynthesis or metabolite conversion, whose biosynthesis is controlled
CC      by endogenous or foreign genes. The method allows control over the time
CC      and rate of gene expression either throughout the whole plant, or in
CC      localized tissues, to achieve e.g. fungal or insect resistance by for
CC      instance dusting the leaves with the chemical regulator. Controlling the
CC      developmental processes by the application of a regulating chemical in
CC      e.g. the commercial production of cultivated crops allows processes such

```

```

CC      as germination, flower formation and fruit ripening to be synchronised at
CC      a given time.
XX
SQ      Sequence 653 BP; 165 A; 114 C; 157 G; 215 T; 2 other;
XX
Alignment Scores:
Pred. No.: 3,73e-53 Length: 653
Score: 473.50 Matches: 90
Percent Similarity: 88.33% Conservative: 16
Best Local Similarity: 75.00% Mismatches: 10
Query Match: 78.01% Indels: 4
DB: Query Match: 20 Gaps: 1

US-09-786-715-4 (1-118) x AAV62799 (1-653)
Qy      3 SerSergLugLugLugLugValAlleGlyCysHisSerValAspGluTrpLysGluInphe 22
Db      69 TCATCCGAGGAGGACGACAAAGTGTTCGCTGCCCAAGGTTGAGAGAAATGAAACGACTTTC 128
Qy      23 GlnLysGlyValAspSerLysLysLeuValAlleAspPheThrAlaSerTrpCysGly 42
Db      129 AAGAAAGGCGTTGAACACTAAGAACTGGTGGTGATTTTACTGCTCATGTGTCGGS 188
Qy      43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
Db      189 CCTGCCGTTTATGCCCCCAATCTGCTGACATTGCTGTAAGACAGTGGCCCATGTTATA 248
Qy      63 PheleulsValAspValAspGluLeuLysThrValAlaA-GluGluPheLysValGluAl 82
Db      249 TTCTCCAAAGGTTGATGTTGATGACACTGTTTCAGCGGCAATGAGTGGAGGCG 308
Qy      82 aMeProThrPheValPheLeuLysGluGlyLysGluValGluATGLeuValGlyAlaAr 102
Db      309 AATGCCAATTGTTGCTTCATTAAAGATGGAAGAGAGTGGACAGAGTGTGGGCCAA 368
Qy      102 gLysGluGluLeuGlnAlaThrValGluLysHisGlyAlaA-----lIeThrAla 118
Db      369 GAAAGAGGAGTTGCAGCAGACCATATGTAAGACATGCTGCTGCTACTGTCATGCT 426

RESULT 4
AAV81683 standard; DNA; 653 BP.
XX
AC      AAV81683;
XX
DT      25-FEB-1999 (first entry)
XX
DE      Tobacco protein-synthesis independent gene pl.4.3.
XX
KW      Regulation; transcription; plant tissue; chimeric construction; PR;
KM      pathogenesis-related protein; anti-pathogenic; transgenic plant;
KW      beta-L-1,3-glucanase activity; pest resistance; ss.
XX
OS      Nicotiana sp.
XX
PN      US5847258-A.
XX
PD      08-DEC-1998.
XX
PF      31-MAY-1995; 95US-0457364.
XX
PR      31-MAY-1995; 95US-0457364.
XX
PR      08-MAR-1998; 89US-0165667.
XX
PR      06-FEB-1988; 89US-0305566.
XX
PR      24-MAR-1989; 89US-0329018.
XX
PR      20-JUN-1989; 89US-036672.
XX
PR      20-OCT-1989; 89US-0425504.
XX
PR      07-SEP-1990; 90US-0580431.
XX
PR      21-DEC-1990; 90US-0632441.
XX
PR      01-APR-1991; 91US-0678378.
XX
PR      27-SEP-1991; 91US-0768122.
XX
PR      06-MAR-1992; 92US-0848506.
XX
PR      06-NOV-1992; 92US-0973197.

```

PR 06-APR-1993; 93US-0042847.
PR 12-APR-1993; 93US-0045957.
PR 16-JUL-1993; 93US-0093301.
PR 13-JAN-1994; 94US-0181271.
XX
PA (NOVS) NOVARTIS FINANCE CORP.
XX
PI Moyer MB, Payne GB, Ryals JA, Ward ER;
XX
XX WPI: 1999-059180/05.
XX
PT DNA encoding pathogenesis-related glucanase proteins - useful for
PT producing transgenic plants with enhanced disease or pest resistance
XX
XX Example 40; Column 253-254; 169pp: English.
XX
XX The present invention describes a DNA molecule encoding a
CC pathogenesis-related (PR) protein having beta-1,3-glucanase activity
CC selected from PR-2, PR-2', PR-2'', PR-N, PR-O and PR-O'. Also described
CC are: (i) a chimeric gene comprising the above DNA molecule linked to a
CC heterologous promoter; (ii) a vector containing the chimeric gene;
CC (iii) a host cell containing the chimeric gene; (iv) a transgenic plant
CC containing the chimeric gene; and (v) a seed from the transgenic plant.
CC The DNA molecule is used to produce transgenic plants with enhanced
CC disease or pest resistance. The present sequence represents a tobacco
CC protein-synthesis independent gene pI.4.3 from the present invention.
XX
SQ Sequence 653 BP; 165 A; 114 C; 157 G; 215 T; 2 other:

Alignment Scores:
Pred. No.: 3,73e-53 Length: 653
Score: 473.50 Matches: 90
Percent Similarity: 88.33% Conservative: 16
Best Local Similarity: 75.00% Mismatches: 10
Query Match: 78.01% Indels: 4
DB: 20 Caps: 1

US-09-786-715-4 (1-118) x AAV81683 (1-653)
QY 3 SerSerGIuGIuGIuValIIeGIuCySHisSerValAspGIuTrpLysGIuGlnPhe 22
Db 69 TCATCCGAGGAGGACAGCTTCGGCTGCCACAGGTTGAGCATGAGACAGACTCTTC 128
QY 23 GlnLysGIuValAspSerLysLysLeuValValIIeAspPheThrAlaSerTrpCysGly 42
Db 129 AAGAAAGCGCTTGAAGTAAAGAACTGGTGGTGGTCTGATTTACTGCTTCATGTCGGGS 188
QY 43 ProCysArpPheIleAlaProIleLeuAlaGluMetAlaLysTrpPheHisValIle 62
Db 189 CCTTCCCGTTTATGCCCCAATTCCTGACATTCGTAAGAAGATGCCCATGTTATA 248
QY 63 PheLeuLysValAspValAspGIuLeuLysThrValAla-GluGIuPheLysValGluAla 82
Db 249 TTCCTCAGGTTATGTGATGAACTGAACGACGCTTCACCGGGAGATGGAGTGGAGGC 308
QY 82 aMetProItrPheValPheLeuLysGluLysGIuValGluArgLeuValGluAla 102
Db 309 AAGCCAACTTTTGTCTTCATTAAAGATGAAAAAGAGTGCACAGATGTTGTGTCCAA 368
QY 102 GlySGluGIuLeuGluAlaThrValGluLysHisGlyAla-----IlePheAla 118
Db 369 GAAAGAGGAGTTCACACAGACACATGATGAGCATGCTGCTCTCTACTGTCTACTGCT 426

RESULT 5
AA251740
ID AA251740 standard; cDNA; 601 BP.
XX
AC AA251740:
XX
XX 04-JUL-2000 (first entry)
XX
DE Glycine max thioredoxin cDNA-2.
XX

KW Glycine max thioredoxin; clone sfil.pk0029.e2; chimeric gene; soybean;
KW transgenic plant; seed storage protein; allergenicity; ss.
XX
XX Glycine max.
XX
XX Key Location/Qualifiers
FT CDS 37..408
FT /*tag= a
FT /product= "Thioredoxin"
XX
XX WO200014239-A2.
XX
XX 16-MAR-2000.
XX
XX 07-SEP-1999; 99WO-US20420.
XX
XX 08-SEP-1998; 98US-0099501.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Allen SM, Thorpe CJ, Lu AL;
XX
XX WPI: 2000-256987/22.
XX
XX P-PSDB: AAY70482.
XX
XX New isolated polynucleotide encoding thioredoxin polypeptide is useful
PT for producing transgenic plants with an altered level of thioredoxin -
PT
XX
XX Claim 3; Page 30-31; 33pp: English.
XX
XX The present cDNA sequence encodes glycine max thioredoxin protein. The
CC cDNA was derived from clone sfil.pk0029.e2, which was isolated from a
CC cDNA library prepared from soybean immature flower. Chimeric genes
CC encoding all or a portion of the thioredoxin protein, in sense or
CC antisense orientation are constructed, wherein expression of the chimeric
CC gene results in production of altered levels of the thioredoxin protein
CC in a transformed host cell. Thioredoxin is involved in the disassembly of
CC seed storage proteins during germination by reducing S-S bonds and in the
CC bread making process. Over expression of thioredoxin in cereals may
CC reduce the allergenicity of any transgenic protein engineered into
CC cereal crops with high sulphydryl content.
XX
SQ Sequence 601 BP; 194 A; 103 C; 136 G; 168 T; 0 other:

Alignment Scores:
Pred. No.: 1,47e-49 Length: 601
Score: 446.00 Matches: 80
Percent Similarity: 85.59% Conservative: 21
Best Local Similarity: 67.80% Mismatches: 17
Query Match: 73.48% Indels: 0
DB: 21 Caps: 0

US-09-786-715-4 (1-118) x AA251740 (1-601)
QY 1 MetAlaSerSerGIuGIuGIuValIIeGIuCySHisSerValAspGIuTrpLysGIu 20
Db 37 ATGGCTGAAGTGAAGAGGAGGACGTCATCGCGCTCCACACCGTTGATGAGTGAAGCTG 96
QY 21 GlnPheGlnLysGIuValAspSerLysLysLeuValValIIeAspPheThrAlaSerTrp 40
Db 97 CAACCTCCAGAAAGCAAAAGCAATGATGATGATGATGATGATGATGATGATGATGATG 156
QY 41 CysGIuProCysArpPheIleAlaProIleLeuAlaGluMetAlaLysTrpPheHis 60
Db 157 TGTGTCATTCGCGTTTATGCCCCAAGTTCCTTCAGAGATGTCACAAAGAACTCTGAA 216
QY 61 ValIIePheLeuLysValAspValAspGIuLeuLysThrValAlaGluPheLysVal 80
Db 217 TTGATCTTCCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 276
QY 81 GluAlaMetProItrPheValPheLeuLysGIuLysGIuValGluArgLeuValGly 100
Db 277 GAGGCCATCCAAACCTTCCTTCTTGAAGAAGATGCCAGATGCTGGACAAAGGTGGTGGT 336

OY		101	AAGTGGGCGCCTTCACCCACCATGCATGCATTGCTTTGCT	118
Dd		337	GCTAGTAGAGGATCACTTCACGCCACCATGCATGCATTGCTTTGCT	350
RESULT 6				
ID	ABX18045	standard; cDNA; 392 BP.		
XX	ABX18045;			
XX	ABX18045;			
DT	10-FEB-2003	(first entry)		
XX				
DE	Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #102.			
KW	Human: GDP-mannose 4,6-dehydratase; GM4,6D: gene; ss: inflammation;			
KM	cellular fucosylation; glycoconjugate fucosylation; transplant rejection;			
KW	arthritis; asthma; sepsis; reperfusion injury; stroke; infection;			
KM	complex carbohydrate; gene replacement therapy; immunosuppressive;			
KW	antiinflammatory; antiarthritic; antibacterial; cerebroprotective;			
KM	antialstmatic; vasotropic.			
OS	Homo sapiens.			
XX				
PN	U52002110548-A1.			
PD	15-AUG-2002.			
PF	11-JUN-2001; 2001US-0876574.			
XX				
PR	22-NOV-1996; 96US-0753323.			
PR	03-DEC-1997; 97US-0984246.			
PR	09-SEP-1998; 98US-0149674.			
PR	14-JUN-1999; 99US-0333177.			
PA	(GENE) GENETICS INST INC.			
PI	Sullivan F, Kriz R, Kumar R;			
DR	WPI; 2003-066673/06.			
PT	New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)			
PT	peptide, for manufacturing complex carbohydrates, or as targets for			
PT	screening GM4,6D antagonists for treating e.g. arthritis, or transplant			
PS	rejection -			
XX				
XX	Disclosure; SEQ ID NO 104; 6pp; English.			
CC	The invention relates to a composition comprising a human GDP-mannose			
CC	4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying			
CC	GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation			
CC	in a mammalian subject and for treating or ameliorating diseases affected			
CC	by the level of cellular fucosylation or diseases affected by the			
CC	fucosylation of glycoconjugates. These diseases include arthritis,			
CC	transplant rejection, asthma, sepsis, reperfusion injury, stroke or			
CC	infection. The GM4,6D peptide or a polynucleotide encoding it is also			
CC	useful for manufacturing complex carbohydrates and as targets for			
CC	screening small molecule antagonists of the activity of the enzyme. The			
CC	polynucleotide is useful in developing an assay for defects in the			
CC	enzyme, as well as in gene replacement therapy. Sequences			
CC	ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding			
CC	human GM4,6D peptides of the invention.			
CC	Note: The sequence data for this patent did not form part of the printed			
CC	specification but was obtained in electronic format directly from USPRO			
CC	at seqdata.uspro.gov/sequence.html.			
XX				
SQ	Sequence 392 BP; 99 A; 80 C; 107 G; 106 T; 0 other:			
Alignment Scores:				
Pred. No.:	1.28e-48	Length:	392	
Score:	437.00	Matches:	77	
Percent Similarity:	86.09%	Conservative:	22	
Best Local Similarity:	66.96%	Mismatches:	16	

Query Match:	71.99%	Indels:	0
DB:	25	Gaps:	0
US-09-786-715-4 (1-118) x ABX18045 (1-392)			
QY	4 SerGIuGIuGIyGIuValIIleGIyCysHisSerValAspGIuTrPlySGluGlnPheGln	23	
Db	9 GCTAAGAGGGGTCAAGGTGTGGCGCTCCACACCCCTTGATGGCTGGAGACCACTGCAG	68	
QY	24 LysGIyValAspSerLysLysLeuValValIIleAspPheThrAlaSerTrpCysGIyPro	43	
Db	69 AATGGAAGAGACTCCCAAAATATGATGTGGTGGATTTTACTGCTCTCTGGTGGTCA	128	
QY	44 CysArpPheIIleAlaProlIIleLeuAlaGluMetAlaLysLysTrpProHisValIIlePhe	63	
Db	129 TGCCGTTTATTTGGCCCAAGTCTGGCAGAGATTTCTAGGCACTACTCCTCAAGTATCTTC	188	
QY	64 LeuLysValAspValAspGIuLeuLysThrValAlaGluGluPheLysValGIuAlaMet	83	
Db	189 CTCAGAGGTGATGGATGGAAGTGAAGCGCTGTGCTGAGGAATTTCCATGTAGGCCATG	248	
QY	84 ProThrPheValPheLeuLysGIuGIyLysGIuValGluArgLeuValGIyAlaArgLys	103	
Db	249 CCAACCTTCCCTCTTGAAAGATGGCAAGATCGTGATAGGTGGTGGTGAAG	308	
QY	104 GluGluLeuGlnAlaThrValGluLysHisGlyAlaIleThrAla	118	
Db	309 GAGAGCTGCACACTCACCATATGACCAACATGATATCTGCTGCT	353	
RESULT 7			
ABX21664			
ID	ABX21664 standard; cDNA: 402 BP.		
XX	ABX21664;		
AC			
XX	10-FEB-2003 (first entry)		
DT			
XX			
DE	Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #3721.		
XX			
KW	Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;		
KW	cellular fucosylation; glycoconjugate fucosylation; transplant rejection;		
KW	arthritis; asthma; sepsis; reperfusion injury; stroke; infection;		
KW	complex carbohydrates; gene replacement therapy; immunosuppressive;		
KW	antiinflammatory; antiarthritic; antibacterial; cerebroprotective;		
XX	antislumatic; vasotropic.		
XX			
OS	Homo sapiens.		
XX			
XX	US2002110548-A1.		
XX			
XX	15-AUG-2002.		
XX			
XX	11-JUN-2001; 2001US-0878574.		
XX			
PR	22-NOV-1996; 96US-0753233.		
PR	03-DEC-1997; 97US-0984246.		
PR	09-SEP-1998; 98US-0149674.		
PR	14-JUN-1999; 99US-0333177.		
XX			
PA	(GEMV) GENETICS INST INC.		
XX			
PI	Sullivan F, Kriz R, Kumar R;		
XX			
DR	WPI; 2003-066673/06.		
XX			
PT	New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)		
PT	peptide, for manufacturing complex carbohydrates, or as targets for		
PT	screening GM,6D antagonists for treating e.g. arthritis, or transplant		
PT	rejection		
XX			
PS	Disclosure; SEQ ID NO 3723; 6pp; English.		
XX			
CC	The invention relates to a composition comprising a human GDP-mannose		

CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
CC GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation
CC in a mammalian subject and for treating or ameliorating diseases affected
CC by the level of cellular fucosylation or diseases affected by the
CC fucosylation of glycoconjugates. These diseases include arthritis,
CC transplant rejection, asthma, sepsis, reperfusion injury, stroke or
CC infection. The GM4,6D peptide or a polynucleotide encoding it is also
CC useful for manufacturing complex carbohydrates and as targets for
CC screening small molecule antagonists of the activity of the enzyme. The
CC polynucleotide is useful in developing an assay for defects in the
CC enzyme, as well as in gene replacement therapy. Sequences
CC ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding
CC human GM4,6D peptides of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 402 BP; 113 A; 76 C; 122 G; 91 T; 0 other;

Alignment Scores:
Pred. No.: 3,32e-48 Length: 402
Score: 434.00 Matches: 79
Percent Similarity: 86.61% Conservative: 18
Best Local Similarity: 70.54% Mismatches: 15
Query Match: 71.50% Indels: 0
DB: Gaps: 0

US-09-786-715-4 (1-118) x ABX21664 (1-402)
QY 4 SerGluGluGlnValIleGlyCysHisSerValAspGluTyrPlyGluGlnPheGln 23
DB 46 GCGGAAAGGAGCAAGTATCGGTGTCACAGCTAAGAGGTGGAAGCAATCTCAAG 105
QY 24 LysGlyValAspSerLysLeuValValIleAspPheThrAlaSerTPCysGlyPro 43
DB 106 AAGGAGAGAGAGTCCAAATATGATCTGCTGATTTACTGCTTTGCGGCTCCA 165
QY 44 CysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIlePhe 63
DB 166 TGGCGTTTCATGGCCCAATCTTCGACAGATTGCTAAAGATTGCCGAATGTCACCTTC 225
QY 64 LeuLysValAspValAspGluLeuLysThrValAlaGluGluPheLysValAlaIleMet 83
DB 226 CTCACCTGATGATGGATGATGAGACTGTTTCCAAAGGTGGGAATTTAGAGCTATG 285
QY 84 ProThrPheValPheLeuLysGluGlyLysGluValGluArgLeuValGlyAlaArgLys 103
DB 286 CCAAGCTTCTGTTCTTGAAGAAGCAAGCTGCTGCAACAAGTTGGGTGCCAACA 345
QY 104 GluGluLeuGlnAlaThrValGluLysHisGlyAla 115
DB 346 GACGAGCTGCATTTGACCTTACGACGACATGCGCA 381

RESULT 8
AAH87768
ID AAH87768 standard; cDNA; 509 BP.
XX
XX AAH87768:
XX
XX 25-SEP-2001 (first entry)
XX
XX Peppermint plant oil gland expressed cDNA 124.
XX
XX Peppermint plant oil gland cell; terpenoid essential oil; resin;
XX genetic mapping; antisense suppression; recombinant expression; ss.
OS Mentha x piperita.
XX
XX
XX WO200153319-A1.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001WO-US02567.

XX
PR 20-JAN-2000; 2000US-0177264.
XX
XX (CROT/) CROTAU R. B.
PA (LANG/) LANGE B M.
PA (WILD/) WILDUNG M R.
PI Croteau RB, Lange BM, Wildung MR;
XX
XX WPI: 2001-488706/53.
XX
XX New nucleic acid molecules corresponding to mRNA molecules expressed in
XX peppermint oil glands for enhancing expression of plant oil gland cell
XX proteins -
XX
XX Claim 1; Page 125; 251pp; English.
XX
XX The invention relates to nucleic acid molecules (AAH87645-AAH88116) that
XX correspond to all or part of a mRNA molecule expressed in plant oil
XX gland cells, especially peppermint and plant oil glands that produce
XX terpenoid essential oils and resins. The nucleic acids are useful for
XX genetically mapping a plant genome for genes expressed in plant oil
XX gland cells and to suppress (for example by antisense suppression) or
XX enhance their expression (for example by genetically transforming a
XX plant cell with a replicable expression vector that expresses one or more
XX proteins naturally expressed in plant oil gland cells). The nucleic acids
XX are also useful for recombinant expression of plant oil gland proteins
XX required for terpenoid essential oil and/or resin production in bacterial
XX and/or yeast cells.
XX
SQ Sequence 509 BP; 144 A; 103 C; 129 G; 133 T; 0 other;
XX
XX
Alignment Scores:
Pred. No.: 5,33e-48 Length: 509
Score: 433.50 Matches: 84
Percent Similarity: 85.22% Conservative: 14
Best Local Similarity: 73.04% Mismatches: 15
Query Match: 71.42% Indels: 2
DB: Gaps: 1

US-09-786-715-4 (1-118) x AAH87768 (1-509)
QY 1 MetAlaSerSerGlu---GluGlyGlnValIleGlyCysHisSerValAspGluTyrPly 19
DB 32 ATGCTTCGTCGGAATCTGAAGGACAGTATGCGGCCACACCACTGATACCTGGAC 91
QY 20 GluGlnPheGlnLysGlyValAspSerLysLeuValValIleAspPheThrAlaSer 39
DB 92 GACGAGCTTCAGAGGCGAATGATACACAAGATTGATGATTCGATTCCTCC 151
QY 40 TrpCysGlyProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrPro 59
DB 152 TGGTGGCGGCGCTGTGCTTCATCGGCCCTTTCTTCGCAAGATTTGCCAAGAAAGTTCC 211
QY 60 HisValIlePheLeuLysValAspValAspGluLeuLysThrValAlaGluGluPheLys 79
DB 212 AATGTGACATTTCTCAAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 271
QY 80 ValGluAlaMetProThrPheValPheLeuLysGluGlyLysGluValGluArgLeuVal 99
DB 272 GTGGAGGCAATGCCAATCTTCATCTTCTTCAAGAAGAGAAAGATCTTGGACAGATCGTA 331
QY 100 -GlyAlaArgLysGluGluLeuGlnAlaThrValGluLysHis 113
DB 332 GGGAGCGAAGAAAGAGAGCTGCGCAAGTAATATTGCTTAACAC 374

RESULT 9
ABX19403
ID ABX19403 standard; cDNA; 390 BP.
XX
XX ABX19403:
AC
XX 10-FEB-2003 (first entry)
DT

XX DE Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #1460.
 XX XX
 KW Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;
 KW cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
 KW arthritis; asthma; sepsis; reperfusion injury; stroke; infection;
 KW complex carbohydrate; gene replacement therapy; immunosuppressive;
 KW antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
 KW antiasmatic; vasotropic.
 OS Homo sapiens.
 XX XX
 PN US2002110548-A1.
 XX XX
 PD 15-AUG-2002.
 XX XX
 PF 11-JUN-2001; 2001US-0878574.
 XX XX
 PR 22-NOV-1996; 96US-0753233.
 PR 03-DEC-1997; 97US-0984246.
 PR 09-SEP-1998; 98US-0149674.
 PR 14-JUN-1999; 99US-0333177.
 XX XX
 PA (GENY) GENETICS INST INC.
 XX XX
 PI Sullivan F, Kriz R, Kumar R;
 XX XX
 DR WPI; 2003-066673/06.
 XX XX
 PT New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
 PT peptide, for manufacturing complex carbohydrates, or as targets for
 PT screening GM4,6D antagonists for treating e.g. arthritis, or transplant
 PT rejection
 XX XX
 PS Disclosure: SEQ ID NO 1462; 6pp; English.
 XX XX
 CC The invention relates to a composition comprising a human GDP-mannose
 CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
 CC GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation
 CC in a mammalian subject and for treating or ameliorating diseases affected
 CC by the level of cellular fucosylation or diseases affected by the
 CC fucosylation of glycoconjugates. These diseases include arthritis,
 CC transplant rejection, asthma, sepsis, reperfusion injury, stroke or
 CC infection. The GM4,6D peptide or a polynucleotide encoding it is also
 CC useful for manufacturing complex carbohydrates and as targets for
 CC screening small molecule antagonists of the activity of the enzyme. The
 CC polynucleotide is useful in developing an assay for defects in the
 CC enzyme, as well as in gene replacement therapy. Sequences
 CC ABX17942-ABX17944 and ABX17947-ABX3716 represent DNA molecules encoding
 CC human GM4,6D peptides of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html.
 XX XX
 SQ Sequence 390 BP; 97 A; 86 C; 97 G; 110 T; 0 other;
 Alignment Scores:
 Pred. No.: 1.08e-47 Length: 390
 Score: 430.00 Matches: 77
 Percent Similarity: 88.18% Conservative: 20
 Best Local Similarity: 70.00% Mismatches: 13
 Query Match: 70.84% Indels: 0
 DB: 25 Gaps: 0
 US-09-786-715-4 (1-118) x ABX19403 (1-390)
 OY 1 MetalaserSerGluGlyValIleGlyCysHisSerValAspGluTrpLysGlu 20
 DB 57 ATGGCTGAAGTGGAGAGGACAGCTCATCGCGCCACACCGCTTGATGAGTGGAGCTG 116
 OY 21 GluPheGlnLysGlyValAspSerLysLysLeuValIleAspPheThrAlaSerTrp 40
 DB 117 CAATCTCAGAAATGCAAAAGACTCCAAAACATGATTGGTGGTGGTATTACTCTCTCTGG 176

OY 41 CysGlyProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysTrpProHis 60
 DB 177 TGTGGTCCATGCGGCTTTATGGCCCCAGTCTTGAGAGATTCGCAAGAAACCTCTGAA 236
 OY 61 ValIlePheLeuLysValAspValAspGluLeuLysTrpValAlaGluLupheLysVal 80
 DB 237 TTGATCTTCCTCAAAAGTGGATGTGATGAAAGAGAGCCGTGCTGAGCAATATTCAT 296
 OY 81 GluAlaMetProThrPheValAlaPheLeuLysGlyLysGluValAlaArgLeuValGly 100
 DB 297 GAGGCCATGCCAAACCTTCCTCTCTGAAAGATGCGAGATGTCGACAAAGGTGGTGT 356
 OY 101 AlaArgLysGluGluLeuGluAlaThrVal 110
 DB 357 GCTAGTAAAGATGACCTTCACGCCACATTA 386
 RESULT 10
 AA251739
 ID AA251739 standard; cDNA; 738 BP.
 XX XX
 AC AA251739;
 XX XX
 DT 04-JUL-2000 (first entry)
 XX XX
 DE Glycine max thiorodoxin cDNA-1.
 XX XX
 KW Glycine max thiorodoxin; clone sahlc.pk001.117; chimeric gene; soybean;
 KW transgenic plant; seed storage protein; allergenicity; ss.
 XX XX
 OS Glycine max.
 XX XX
 FH Key Location/Qualifiers
 FT CDS 68..430
 FT /*tag= a
 FT /product= "Thiorodoxin"
 FT FT
 PN MO200014239-A2.
 XX XX
 PD 16-MAR-2000.
 XX XX
 PF 07-SEP-1999; 99WO-US20420.
 XX XX
 PR 08-SEP-1998; 98US-0099501.
 XX XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PI Allen SM, Thorpe CJ, Lu AL;
 XX XX
 DR WPI: 2000-256987/22.
 DR P-PSDB: AAT70481.
 XX XX
 PT New isolated polynucleotide encoding thiorodoxin polypeptide is useful
 PT for producing transgenic plants with an altered level of thiorodoxin -
 XX XX
 PS Claim 3; Page 30; 33pp; English.
 XX XX
 CC The present cDNA sequence encodes Glycine max thiorodoxin protein. The
 CC cDNA was derived from clone sahlc.pk001.117, which was isolated from a
 CC cDNA library prepared from soybean tissue sprayed with authority
 CC herbicide. Chimeric genes encoding all or a portion of the thiorodoxin
 CC protein, in sense or antisense orientation are constructed, wherein
 CC expression of the chimeric gene results in production of altered levels
 CC of the thiorodoxin protein in a transformed host cell. Thiorodoxin is
 CC involved in the disassembly of seed storage proteins during germination
 CC by reducing S-S bonds and in the bread making process. Over expression of
 CC thiorodoxin in cereals may reduce the allergenicity of any transgenic
 CC protein engineered into cereal crops with high sulfhydryl content.
 XX XX
 SQ Sequence 738 BP; 260 A; 120 C; 146 G; 212 T; 0 other;
 Alignment Scores:
 Pred. No.: 2.57e-47 Length: 738


```

FT /number= 2
XX
XX US2002088025-A1.
XX
XX 04-JUL-2002.
XX
XX 03-JUL-2001; 2001US-0897425.
XX
XX 22-FEB-1991; 91US-0659835.
XX 16-NOV-1993; 93US-0142418.
XX 30-DEC-1994; 94US-0366783.
XX 25-APR-1997; 97US-0846021.
XX 18-DEC-1998; 98US-0210843.
XX
XX (MOLO/) MOLONEY M. M.
XX (DALM/) DALMIA B. K.
XX
XX Moloney MM, Dalmia BK;
XX
XX WPI: 2002-635723/68.
XX
XX Expressing protein, by introducing chimeric nucleotide regulatory
XX sequence, sequence encoding fusion protein, having sequence encoding
XX protein, oleosin gene and sequence encoding termination region and
XX producing protein -
XX
XX Example 21; Fig 14; 69pp; English.
XX
XX The invention describes a method of expressing thioresdoxin or thioresdoxin
XX reductase (I) in the oil body of a host cell using an oil body protein
XX gene. The method involves introducing a chimeric nucleic acid comprising
XX a first sequence to regulate transcription, a second DNA sequence
XX encoding a fusion polypeptide, comprising a sequence encoding an oleosin
XX gene and sequence encoding (I) and a third sequence encoding a
XX termination region functional in the host cell and growing the host cell
XX to produce a fusion polypeptide. The method or (I) is useful for
XX expression of a thioresdoxin or thioresdoxin reductase by a host cell. This
XX thioresdoxin gene controlled by a phaseolin promoter and phaseolin
XX terminator sequence.
XX
XX Sequence 3888 BP; 1254 A; 722 C; 613 G; 1299 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 5 23e-45 Length: 3888
XX Score: 420.00 Matches: 74
XX Percent Similarity: 85.96% Conservative: 24
XX Best Local Similarity: 64.91% Mismatches: 16
XX Query Match: 69.19% Indels: 0
XX DB: 24 Gaps: 0
XX
XX US-09-786-715-4 (1-118) x ABS53097 (1-3888)
XX
XX 3 SerSerGluGluGlyGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1558 GCTTGGAAGAAGAGCAAGTAGTCCGCCACACCGTTGACACATGACAGACAGACGCT 1617
XX
XX 23 GlnIysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1618 CAGAAGGCTAATGATCCAAACACTCTGTGTGGTGTTCACGCGCTTCTGTGGTGA 1677
XX
XX 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1678 CCAATGCTTTCATGCTCCATCTTTCGTGATTTGGCTAGCAAACTTCTACCTGCTT 1737
XX
XX 63 PheLeuLysValAspValAspGluLeuLysThrValAlaGluGluPheLysValAlaGlu 82
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1738 TTCCTCAAGGTTGATGACTGATGAAATGAGTCGGTGGCAAGTGTGGCCATACAGGGG 1797
XX
XX MetProThrPheValPheLeuLysGluGlyValAlaGluArgLeuValGlyAlaArg 102
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1798 ATGCCAACCTTCATCTTTTGAAGAGAGGAAATTTGGACAAAGTGTGGTGGACCAAG 1857

```

```

OY 103 LysGluGluLeuGlnAlaThrValGluLysHisGlyAlaIle 116
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1858 AAAGATGAGCTTCACGTACCATTCGCCAAACACTTGGCTATG 1899
XX
XX RESULT 13
XX ABN89581
XX ID ABN89581 standard; DNA; 3888 BP.
XX
XX ABN89581;
XX
XX 06-SEP-2002 (first entry)
XX
XX Phaseolin promoter-Trxh oleosin-phaseolin terminator DNA SEQ.19.
XX
XX Multimeric protein; redox protein; thioresdoxin; thioresdoxin reductase;
XX oil body; ophthalmological; antidiabetic; cytosolic; antiproliferic;
XX vasotropic; vulnary; antibacterial; immunosuppressive; antitumor;
XX food product; milk; wheat; oxidative stress; cataract; diabetes;
XX chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
XX bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
XX gastro intestinal bleeding; intestinal bowel disease; ulcer;
XX gastro oesophageal reflux disease; gene; ds.
XX
XX Arabidopsis sp.
XX Phaseolus vulgaris.
XX
XX WO200250289-A1.
XX
XX 27-JUN-2002.
XX
XX 19-DEC-2001; 2001WO-US50240.
XX
XX 19-DEC-2000; 2000US-0742900.
XX 05-JUL-2001; 2001US-302885P.
XX 04-DEC-2001; 2001US-0006038.
XX
XX (SEMB-) SEMBIOSYS GENETICS INC.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
XX Del Val G, Zaplachinski S, Moloney M;
XX
XX WPI: 2002-508806/54.
XX P-PSDB; ABP60683.
XX
XX Producing oil body associated with recombinant multimeric protein
XX complex e.g. redox proteins and immunoglobulins comprises producing
XX recombinant polypeptides capable of forming the complex in cells
XX comprising oil bodies -
XX
XX Example 2; Page 169-171; 362pp; English.
XX
XX The present invention describes a method (M1) for producing an oil body
XX associated with a recombinant multimeric protein complex (MPC). M1
XX comprises producing in a cell comprising oil bodies a first and second
XX recombinant polypeptide (P1, P2), where P1 is capable of associating
XX with P2 to form the MPC and associating the complex with an occlusion
XX body (OB) through an OB-targeting-protein capable of associating with OB
XX and P1. M1 is useful for producing an oil body associated with a
XX recombinant MPC. The oil bodies are further formulated for use in the
XX preparation of a food product such as milk or wheat based food product,
XX personal care product which reduces the oxidative stress on the surface
XX area of the human body or used to lighten the skin, or a pharmaceutical
XX composition used to treat chronic obstructive pulmonary disease (COPD),
XX cataracts, diabetes, emphysema, bronchiopulmonary disease, psoriasis,
XX malignancies, reperfusion injury, wound healing, sepsis, gastro
XX intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
XX (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677
XX to ABP60964 represent sequence given in the exemplification of the
XX present invention.
XX
XX Sequence 3888 BP; 1254 A; 722 C; 613 G; 1299 T; 0 other;
XX
XX

```

Alignment Scores: 5.23e-45 Length: 3888
Pred. No.: 420.00 Matches: 74
Score: 85.96% Conservative: 24
Best Local Similarity: 64.91% Mismatches: 16
Query Match: 69.19% Indels: 0
DB: 24 Gaps: 0
US-09-786-715-4 (1-118) x ABN89581 (1-3888)
QY 3 SerSerGIuGIuGIuValIleGIuYHisSerValAspGIuTrpLyGIuGlnPhe 22
Db 1558 GCTTCGGAAGAAGACAGATGATCGCTGCCACACCTTGAGACATGGAACGACACCTT 1617
QY 23 GlnLysGIuValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
Db 1618 CAGAGGCTAATGATCAAAACCTTGCTGGTGTATTCACGGCTTCTGGTGTGA 1677
QY 43 ProCysArgPheIleAlaProIleLeuAlaGIuMetAlaLysLysThrProHisValIle 62
Db 1678 CCATGTCGTTTCATCGCTCATCTTCTTGATTTGGCTAAGAACTTCTTAACGCTCT 1737
QY 63 PheLeuLysValAspValAspGIuLeuLysThrValAlaGIuGlnPheLysValIleAla 82
Db 1738 TTCCTCAAGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1797
QY 83 MetProThrPheValPheLeuLysGIuLysGIuValGluArgLeuValGlyAlaArg 102
Db 1798 ATGCCAACCTTCACTTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1857
QY 103 LysGIuGlnLeuGlnAlaThrValGluLysHisGlyAlaIle 116
Db 1858 AAGATGAGCTTCACTTACATTTGCCAACACTTGGCTATG 1899
RESULT 14
ABZ12358 standard; DNA: 345 BP.
XX ID ABZ12358 standard; DNA: 345 BP.
XX AC ABZ12358;
XX DT 21-JAN-2003 (first entry)
XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 163.
XX KM Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX OS Arabidopsis thaliana.
XX PN W0200216655-A2.
XX XX 28-FEB-2002.
XX PF 24-AUG-2001; 2001MO-US26685.
XX PR 24-AUG-2000; 2000US-227866P.
XX PR 26-JAN-2001; 2001US-26464P.
XX PR 22-JUN-2001; 2001US-300111P.
XX PA (SCRI) SCRIPPS RES-INST.
XX PA (SYGN) SYGNEMTA PARTICIPATIONS AG.
XX PI Harper JF, Kreps J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
XX DR WPI; 2002-304127/34.
XX PT Identifying a stress condition to which a plant cell has been exposed
XX PT and producing plants with increased tolerance to these abiotic stresses
XX PT
XX PS Claim 144; SEQ ID NO 163; 577bp + Sequence Listing; English.
XX CC The invention relates to identifying a stress condition to which a plant
XX CC cell has been exposed, comprising:

CC (a) contacting nucleic acid representative of expressed polynucleotides
CC in the plant cell with an array or probes representative of the plant
CC cell genome; and
CC (b) detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.
XX SQ Sequence 345 BP; 90 A; 68 C; 90 G; 97 T; 0 other;
Alignment Scores: 2.63e-46 Length: 345
Pred. No.: 419.00 Matches: 73
Score: 86.49% Conservative: 23
Best Local Similarity: 65.77% Mismatches: 15
Query Match: 69.03% Indels: 0
DB: 24 Gaps: 0
US-09-786-715-4 (1-118) x ABZ12358 (1-345)
QY 3 SerSerGIuGIuGIuValIleGIuYHisSerValAspGIuTrpLyGIuGlnPhe 22
Db 4 GCTTCGGAAGAAGACAGATGATCGCTGCCACACCTTGAGACATGGAACGACACCTT 63
QY 23 GlnLysGIuValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
Db 64 CAGAGGCTAATGATCAAAACCTTGCTGGTGTATTCACGGCTTCTGGTGTGA 123
QY 43 ProCysArgPheIleAlaProIleLeuAlaGIuMetAlaLysLysThrProHisValIle 62
Db 124 CCATGTCGTTTCATCGCTCATCTTCTTGATTTGGCTAAGAACTTCTTAACGCTCT 183
QY 63 PheLeuLysValAspValAspGIuLeuLysThrValAlaGIuGlnPheLysValIleAla 82
Db 184 TTCCTCAAGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
QY 83 MetProThrPheValPheLeuLysGIuLysGIuValGluArgLeuValGlyAlaArg 102
Db 244 ATGCCAACCTTCACTTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 303
QY 103 LysGIuGlnLeuGlnAlaThrValGluLysHis 113
Db 304 AAGATGAGCTTCACTTACATTTGCCAACACTTGGCTATG 336
RESULT 15
ABN89587 standard; DNA: 345 BP.
XX ID ABN89587 standard; DNA: 345 BP.
XX AC ABN89587;
XX DT 06-SEP-2002 (first entry)
XX DE Arabidopsis thaliana thioedoxin h (Trx h 1) DNA SEQ ID NO:38.
XX KM Arabidopsis thaliana thioedoxin h (Trx h 1) DNA SEQ ID NO:38.
XX KM Multimeric protein; redox protein; thioedoxin; thioedoxin reductase;
XX KM oil body; ophthalmological; antidiabetic; cytoskeletal; antipsoriatic;
XX KM vasotropic; vulnery; antibacterial; immunosuppressive; antilucer;
XX KM food product; milk; wheat; oxidative stress; cataract; diabetes;
XX KM chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
XX KM bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;
XX KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
XX KM gastro oesophageal reflux disease; gene; ds.
XX OS Arabidopsis thaliana.
XX PN W0200250289-A1.
XX XX 27-JUN-2002.

XX 19-DEC-2001; 2001MO-US50240.
PF 19-DEC-2000; 2000US-0742900.
PR 05-JUL-2001; 2001US-302885P.
PR 04-DEC-2001; 2001US-0006038.
XX
PA (SEMB-) SEMBIOSYS GENETICS INC.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK.
PI Del Val G, Zaplachinski S, Moloney M.
XX
DR WPI: 2002-508806/54.
DR P-PSDB; ABP60696.
XX
XX Producing oil body associated with recombinant multimeric protein
PT complex e.g. redox proteins and immunoglobulins comprises producing
PT recombinant polypeptides capable of forming the complex in cells
PT comprising oil bodies -
XX
XX Claim 68; Page 197; 362pp; English.
PS
XX
CC The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating
CC with P2 to form the MPC and associating the complex with an occlusion
CC body (OB) through an OB-targeting-protein capable of associating with OB
CC and P1. M1 is useful for producing an oil body associated with a
CC recombinant MPC. The oil bodies are further formulated for use in the
CC preparation of a food product such as milk or wheat based food product,
CC personal care product which reduces the oxidative stress on the surface
CC area of the human body or used to lighten the skin, or a pharmaceutical
CC composition used to treat chronic obstructive pulmonary disease (COPD),
CC cataracts, diabetes, envenomation, bronchiopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677
CC to ABP60964 represent sequence given in the exemplification of the
CC present invention.
XX
SQ Sequence 345 BP; 90 A; 68 C; 90 G; 97 T; 0 other;

Alignment Scores:
Pred. No.: 2.63e-46 Length: 345
Score: 419.00 Matches: 73
Percent Similarity: 86.49% Conservative: 23
Best Local Similarity: 65.77% Mismatches: 15
Query Match: 69.03% Indels: 0
DB: 24 Gaps: 0

US-09-786-715-4 (1-118) x ABN89587 (1-345)

OY 3 SerSerGluGluGlyValIleGlyCysHisSerValAspGluThrPylGluInpHe 22
Db 4 GCTTGGAGAGAGCAAAAGTGCCTGCCACACCGCTTGAGACATGAGACGACGCTT 63
OY 23 GlnLysGlyValAspSerLysLysLeuValIleAspPheThrAlaSerTrpCysGly 42
Db 64 CAGAAAGGCTAAATCAAAACTCTTGTGGTGTGATTTCACGGCTTCTGTGTGGA 123
OY 43 ProGysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
Db 124 CCAATGCGTTTATCGCTCCATCTTGTGATTGGCTAAGAACTTCTAAGCTGCTT 183
OY 63 PheLeuLysValAspValAspGluLeuLysThrValAlaGluLupheLysValGluAla 82
Db 184 TTCCTCAAGCTGATCATCTGATGATGAAGTCGGTGGCAAGTATGGCGCATACAGCGC 243
OY 83 MetProThrPheValPheLeuLysGluGlyValGluValGluArgLeuValGlyAlaArg 102
Db 244 ATGCCAACCTTATGTTTGAAGAGGAGGAGATTTGGACAAAGTTGTGGAGCCAG 303

OY 103 LysGluGluLeuGlnAlaThrValGluLysHis 113
Db 304 AAAGATGAGCTTCAGTCTACCATTTGCCAAACAC 336

Search completed: August 17, 2003, 19:37:09
Job time: 167.884 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 19:18:57 ; Search time 43.7308 Seconds

(without alignments)
1190.995 Million cell updates/sec

Title: US-09-786-715-4

Perfect score: 607
Sequence: 1 MASSEEGVICHSDVEMKE.....VGARKEELQATVEKGAITA 118

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL-frame_p2n.model -DEV-xlp
-O=/cgn2_1/USPTO/spool/US09786715/runat_11082003.150515.6083/app_query.fasta_1.1052
-DB-issued.patents.NA -QFMT-fastap -SUFFIX-rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09786715.ecgn_1.1.175-@runat_11082003.150515.6083 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents.NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCUTS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	473.5	78.0	653	1	US-08-181-271A-103
2	473.5	78.0	653	1	US-08-449-315-103
3	473.5	78.0	653	1	US-08-444-803-103
4	473.5	78.0	653	1	US-08-449-043-103
5	473.5	78.0	653	1	US-08-456-265A-103
6	473.5	78.0	653	1	US-08-455-416-103
7	473.5	78.0	653	1	US-08-455-244-103
8	473.5	78.0	653	1	US-08-454-876-103
9	473.5	78.0	653	2	US-08-457-364-103
10	473.5	78.0	653	2	US-08-456-262-103
11	473.5	78.0	653	2	US-08-456-240-103
12	473.5	78.0	653	2	US-08-455-736-103

13	473.5	78.0	653	2	US-08-971-217-103	Sequence 103, App
14	473.5	78.0	653	3	US-09-350-600-103	Sequence 103, App
15	362	59.6	369	4	US-09-540-014-1	Sequence 1, Appl1
16	358	59.0	382	4	US-09-540-014-3	Sequence 3, Appl1
17	358	59.0	393	4	US-09-540-014-5	Sequence 5, Appl1
18	249	41.0	557	4	US-09-404-879A-88	Sequence 88, Appl1
19	249	41.0	557	4	US-09-338-933-88	Sequence 88, Appl1
20	249	41.0	557	4	US-09-215-681-88	Sequence 88, Appl1
21	249	41.0	581	4	US-09-601-144-67	Sequence 67, Appl1
22	249	41.0	594	4	US-09-404-879A-87	Sequence 87, Appl1
23	249	41.0	594	4	US-09-338-933-87	Sequence 87, Appl1
24	249	41.0	594	4	US-09-215-681-87	Sequence 87, Appl1
25	249	41.0	601	4	US-09-404-879A-133	Sequence 133, App
26	249	41.0	601	4	US-09-338-933-133	Sequence 133, App
27	249	41.0	624	4	US-09-215-681-133	Sequence 133, App
28	249	41.0	624	3	US-09-385-982-526	Sequence 526, App
29	249	41.0	630	3	US-08-180-371-5	Sequence 5, Appl1
30	249	41.0	630	3	US-08-180-371-17	Sequence 17, Appl1
31	249	41.0	630	5	PCT-US92-05707-5	Sequence 5, Appl1
32	227.5	37.5	318	4	US-09-313-294A-5868	Sequence 5868, Ap
33	222	36.6	605	3	US-09-385-982-485	Sequence 485, App
34	222	36.6	631	3	US-09-385-982-174	Sequence 174, App
35	211.5	34.8	914	1	US-08-386-729A-9	Sequence 9, Appl1
36	209	34.4	123025	4	US-09-113-294A-5840	Sequence 5840, Ap
37	186	30.6	278	4	US-09-328-352-1234	Sequence 1234, Ap
38	182.5	30.1	438	4	US-08-775-978-2	Sequence 2, Appl1
39	181	29.8	564	2	US-09-103-840A-2	Sequence 1022, Ap
40	179.5	29.6	4403765	3	US-09-134-001C-1022	Sequence 1022, Ap
41	179.5	29.6	4411529	3	US-09-134-001C-1022	Sequence 1022, Ap
42	178.5	29.4	336	4	US-09-107-532A-3085	Sequence 3085, Ap
43	172	28.3	339	4	US-09-221-017B-373	Sequence 373, App
44	171	28.2	7096	4	US-08-961-527-226	Sequence 226, App
45	157.5	25.9	2520	4		

ALIGNMENTS

RESULT 1
US-08-181-271A-103
Sequence 103, Application US/08181271A
Patent No. 5614395
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesting, John H.
APPLICANT: Friedlich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271A
FILING DATE: 13-JAN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PL/COC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-181-271A-103

Alignment Scores:
Pred. No.: 7.81e-57 Length: 653
Score: 473.50 Matches: 90
Percent Similarity: 88.33% Conservative: 16
Best Local Similarity: 75.00% Mismatches: 10
Query Match: 78.01% Indels: 4
DB: 1 Gaps: 1

US-09-786-715-4 (1-118) x US-08-181-271A-103 (1-653)

Qy 3 SerSerGluGluGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
Db 69 TCATCCGAGGAGGAGCAAGTGTTCGCTGCCCAAGGTTGAGCAATGGAACGACTACTTC 128
Qy 23 GlnLysGlyValAspSerLysLysLeuValIleAspPheThrAlaSerTrpCysGly 42
Db 129 AAGAAAGCGCTTGAGACTAAAGAACTGGTGGTCGATTTTACTGCTTCATGGTGGG 188
Qy 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
Db 189 CCTGCGGTTTATTTATGCCCATCTCTGCTACACTGTGTAGAAGATGCCCATGTATA 248
Qy 63 PheLeuLysValAspValAspGluLeuLysThrValAla-GluIubPheLysValGluAl 82
Db 249 TTCCTCAAGGTGTGATGTGATGAAGTGAAGTCTTTCAGCGGGAATGAGTGTGAGAGC 308
Qy 82 ametProThrPheValPheLeuLysGluGlyValGluArgLeuValGlyValIleAr 102
Db 309 AATGCCAAGCTTTGTCTTCAATTAAGATGAAGAAAGAGTGAAGAGTGTGGTGC 368
Qy 102 GlySGluGluLeuGlnAlaThrValGluLysHisGlyValA-----IleThrAla 118
Db 369 GAAGAGAGATGTGCAGCAGCAACATAGTGAAGCATGCTGCTCTACTGTACTGCT 426

RESULT 2
US-08-449-315-103
Sequence 103, Application US/08449315
Patent No. 5650505
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harns, Christian
APPLICANT: Melns, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,315
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,847
 FILING DATE: 6-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/632,441
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19825/P1/CCC 1727
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8614
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 653 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-449-315-103

Alignment Scores:
 Pred. No.: 7,81e-57 Length: 653
 Score: 473.50 Matches: 90
 Percent Similarity: 88.33% Conservative: 16
 Best Local Similarity: 75.00% Mismatches: 10
 Query Match: 78.01% Indels: 4
 Gaps: 1

US-09-786-715-4 (1-118) x US-08-449-315-103 (1-653)

QY 3 SerSerGluGluGluValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
 |||||
 DB 69 TCATCCGAGGAGGACAGGTGTCGCGTCGCCACAAAGTTGAGAGATGGAACGAGTACTTC 128
 |||||
 QY 23 GlnLysGlyValAspSerLysLysLeuValIleAspPheThrAlaSerTrpCysGly 42
 ::::|
 DB 129 AAGAAAGCGCTGAGACTAAGAACTGCTGCTGCTTACGCTTCATGCTGCGCGS 188
 ::::|
 QY 43 ProGysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
 |||||
 DB 189 CTTGCGCTTTATGTCGCCCATCTCTGTGACATTCGTAAGAAAGATGCCCATGTATA 248
 |||||

QY 63 PheLeuLysValAspValAspGluLysThrValAla-GluLysPheLysValGlu 82
 |||||
 DB 249 TTCCTCAGAGTTCATGATTCATCACTGAAGACTGTTCCAGCGGAAATGAGTGTGAGGC 308
 |||||
 QY 82 aMetProThrPheValPheLeuLysGluLysGlyValGluArgLeuValGlyAla 102
 |||||
 DB 309 AATGCCAACTTTGCTTCATTAAAGATGGAAGAGTGAAGAGTGTGTTGTCCTCA 368
 |||||
 QY 102 GlySGluGluLeuGlnAlaThrValGluLysHisGlyAla-----IleThrAla 118
 :|||||
 DB 369 GAAAGAGAGTTCAGACAGACCATATGATGATGCTGCTCTGCTACTGTCACGCT 426
 :|||||

RESULT 3
 US-08-444-803-103
 Sequence 103, Application US/08444803
 Patent No. 5654414
 GENERAL INFORMATION:
 APPLICANT: Ryals, John A.
 APPLICANT: Alexander, Danny C.
 APPLICANT: Beck, James J.
 APPLICANT: Duesting, John H.
 APPLICANT: Friedrich, Leslie B.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Harms, Christian
 APPLICANT: Meins, Jr., Frederick
 APPLICANT: Montoya, Alice
 APPLICANT: Moyer, Mary B.
 APPLICANT: Neuhaus, Jean-Marc
 APPLICANT: Payne, George B.
 APPLICANT: Speilson, Christoph
 APPLICANT: Stinson, Jeffrey R.
 APPLICANT: Uknes, Scott J.
 APPLICANT: Ward, Eric R.
 APPLICANT: Williams, Sheriella C.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/444,803
 FILING DATE: 19-MAY-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/181,271
 FILING DATE: 13-JAN-94
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,847

APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-449-043-103

Alignment Scores:
Pred. No.: 7,81e-57 Length: 653
Score: 473.50 Matches: 90
Percent Similarity: 88.338 Conservative: 16
Best Local Similarity: 75.00% Mismatches: 10
Query Match: 78.01% Indels: 4
Gaps: 1

US-09-786-715-4 (1-118) x US-08-449-043-103 (1-653)

OY 3 SerSerGIuGIuGIuGIuValIleGIuGShISerValAspGIuTrPLySGluInphe 22
Db 69 TCATCCGAGAGGAGGACAGTGTTCGCTGCCACAGAGTTGAGAGATGAGACGATCTTC 128
OY 23 GlnYssGIuValAspSerLySLeuValValIleAspPheThrAlaSerTrpYsgly 42
Db 129 AAGAAAGCGGTGAAGTAAGAACTGGTGGTGGATTTTACTGCTTCATGAGTGGCGS 188
OY 43 ProCysArGpheIleAlaProIleuAlaGluMeAlaLysLysThrProHisValIle 62
Db 189 CCTTCCGCTTTATTTGCCCCCAATTTCTGTGATGCTAGAGAAATGCCCATTTTATA 248
OY 63 PheIeuLysValAspValAspGIuLeuLysThrValAla-GluIuPheLysValGluAl 82
Db 249 TTCCCAAGGTGTGATGTGATGAAGACTGTTTCAGCGGGAATGAGTGTGAGAGC 308
OY 82 aMePProthrPheValPheIeuLysGIuGIuValGluuValGluValAlaAr 102
Db 309 AATGCCAAGCTTTGCTTCATTAAAGATGAAAGAAAGTGGACAGAGTTGGTGGCCAA 368
OY 102 gLysGIuGIuLeuGlnAlaThrValGIuLysHisGIuAla-----IleThrAla 118
Db 369 GAAGAGAGAGTTGCAGCAGACCAATATGTAAGACATCTCTCTCTACTGTCTACTGCT 426

RESULT 5

US-08-456-265A-103
Sequence 103, Application US/08456265A
Patent No. 5767369
GENERAL INFORMATION:
APPLICANT: Alexander, Danny C.
APPLICANT: Ryals, John A.
APPLICANT: Goodman, Robert M.
APPLICANT: Stinson, Jeffrey R.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,265A
FILING DATE: 31-MAY-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:

LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-456-265A-103

Alignment Scores:
Pred. No.: 7.81e-57 Length: 653
Score: 473.50 Matches: 90
Percent Similarity: 88.33% Conservative: 16
Best Local Similarity: 75.00% Mismatches: 10
Query Match: 78.01% Indels: 4
DB: 1 Gaps: 1

US-09-786-715-4 (1-118) x US-08-456-265A-103 (1-653)

QY 3 SerSerGlnGlnGlnGlnValIleGlyCysHisSerValAspGluTrpGluGlnPhe 22
DB 69 TCATCCGAGGAGGAGACAGTGTTCGGCTGCCACAGAGTGAGGAGGAGGAGTACTTC 128
QY 23 GlnGlyGlyValAspSerLysLysLeuValIleAspPheThrAlaSerTPCysGly 42
DB 129 AAGAAAGCGCTTAGACTAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 188
QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
DB 189 CATTGCCGTTTATGTCCTGACATTCCTGATGATGATGATGATGATGATGATGATGATG 248
QY 63 PheLeuLysValAspValAspGluLeuLysThrValAla-GluGluPheLysValGluAl 82
DB 249 TTCTCAAGGTATGTGTGATGAGACGTAAGACGTCGTACCGGGAAGAGTGTGAGGC 308
QY 82 ametProthrPheValPheLeuLysGluGlyGluValGluAlaArgLeuValGluAlaAr 102
DB 309 AATGCCAAGCTTTGCTCTCTCTTAAGATGAGAAAGAGTGCAGAGAGTGTGCTGCA 368
QY 102 glysGluGluLeuGlnAlaThrValGluLysHisGlyAla-----IleThrAla 118
DB 369 GAAAGAGAGAGTTCACAGACACATAGTAGAGCATGCTGCTGCTGCTGCTGCTGCTGCT 426

RESULT 6
US-08-455-416-103
Sequence 103, Application US/08455416
Patent No. 5777200
GENERAL INFORMATION:
APPLICANT: Rivals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesling, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericoa C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-455-416-103
Alignment Scores:
Pred. No.: 7.81e-57 Length: 653
Score: 473.50 Matches: 90
Percent Similarity: 88.33% Conservative: 16


```

Best Local Similarity: 75.00%      Mismatches: 10
Query Match: 78.01%      Indels: 4
DB: 1      Gaps: 1

US-09-786-715-4 (1-118) x US-08-455-416-103 (1-653)

QY 3 SerSerGIuGIuGIuGIuValIleGIuCYSHISerValAspGIuTrpLySGIuInPhe 22
   |||||
Db 69 TCATCCGGAGGGGCAAGGTCTTCGGCTGCACCAAGCTTGAGAGAAAGGAACGAGTCTCTC 128
   |||||

QY 23 GlnTySValAspSerTyrSylSylSylValValIleAspPheThrLAserTrpCYSGI 42
   ::|||
Db 129 AAGAAAGCGCTTGAGACTTAAGAAACTGGTGGTGGTGCATTTTACTGCTTCAATGTCGG 188
   ::|||

QY 43 ProCYArPheIleAlaProIleLeuAlaGluMetAlaLysSylThrProHisValIle 62
   CCTTGCCGCTTTATGTCGCCCAATCTTGCTGTGACATTCCTAAAGAAATGCCCATGTTATA 248
   |||||

QY 63 PheIleuValAspValAspGIuLeuLysThrValAla-GluGIuPheLysValGlu 82
   |||||
Db 249 TTCCTCAAGGTGTGAATGTGATGACATGAAAGACTGTTCTCCGCGGATGAGTGGAGGC 308
   |||||

QY 82 AmeProThrPheValPheLeuValSylGIuLysGIuValGluArGIuValGIuAla 102
   |||||
Db 309 AATGCCAATTTTGTCTTCTTATTAAGATGGAAAGAGTGGACAGAGTGTGGTCCAA 368
   |||||

QY 102 gLySGIuLLeuGlnAlaThrValGIuLysHISGIuAla-----IleThrAla 118
   :|||
Db 369 GAAAGAGAGTTCGACAGACCATATGTGAACATGCTGCTCCTGCTACTGCTACTGCT 426
   :|||

RESULT 7
US-08-455-244-103
: Sequence 103, Application US/08455244
: Patent No. 5789214
: GENERAL INFORMATION:
: APPLICANT: Ryals, John A.
: APPLICANT: Alexander, Danny C.
: APPLICANT: Beck, James J.
: APPLICANT: Duesing, John H.
: APPLICANT: Friedrich, Leslie B.
: APPLICANT: Goodman, Robert M.
: APPLICANT: Harms, Christian
: APPLICANT: Meins, Jr., Frederick
: APPLICANT: Montoya, Alice
: APPLICANT: Moyer, Mary B.
: APPLICANT: Neuhaus, Jean-Marc
: APPLICANT: Payne, George B.
: APPLICANT: Sperison, Christoph
: APPLICANT: Stinson, Jeffrey R.
: APPLICANT: Uknes, Scott J.
: APPLICANT: Ward, Eric R.
: TITLE OF INVENTION: Williams, Shericca C.
: TITLE OF INVENTION: CHEMICAL REGULATABLE AND ANTI-PATHOGENIC
: NUMBER OF SEQUENCES: 106
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CIBA-GEIGY Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: New York
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/455,244
: FILING DATE: 31-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/181,271

```

```

1 FILING DATE: 13-JAN-94
2 APPLICATION NUMBER: US 08/093,301
3 FILING DATE: 16-JUL-1993
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: US 07/937,197
6 FILING DATE: 6-NOV-1992
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: US 07/678,378
9 FILING DATE: 1-APR-1991
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 07/305,566
12 FILING DATE: 6-FEB-1989
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/165,667
15 FILING DATE: 8-MAR-1988
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 08/042,847
18 FILING DATE: 6-APR-1993
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 07/632,441
21 FILING DATE: 21-DEC-1990
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 07/425,504
24 FILING DATE: 20-OCT 1989
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 07/848,506
27 FILING DATE: 6-MAR-1992
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 07/768,122
30 FILING DATE: 27-SEP-1991
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 07/580,431
33 FILING DATE: 7-SEP-1990
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: US 07/368,672
36 FILING DATE: 20-JUN-1989
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: US 07/329,018
39 FILING DATE: 24-MAR-1989
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 08/045,957
42 FILING DATE: 12-APR-1993
43 ATTORNEY/AGENT INFORMATION:
44 NAME: Elmer, James Scott
45 REGISTRATION NUMBER: 36,129
46 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
47 TELECOMMUNICATION INFORMATION:
48 TELEPHONE: (919)541-8614
49 TELEFAX: (919)541-8689
50 INFORMATION FOR SEO ID NO: 103:
51 SEQUENCE CHARACTERISTICS:
52 LENGTH: 653 base pairs
53 TYPE: nucleic acid
54 STRANDEDNESS: single
55 TOPOLOGY: linear
56 MOLECULE TYPE: DNA (genomic)
57 US-08-455-244-103
58
59 Alignment Scores:
60 Pred. No: 7,81e-57 Length: 653
61 Score: 473.50 Matches: 90
62 Percent Similarity: 88.33% Conservative: 16
63 Best local Similarity: 75.00% Mismatches: 10
64 Query Match: 78.01% Indels: 4
65 DB: 1 Gaps: 1
66
67 US-09-786-715-4 (1-118) x US-08-455-244-103 (1-653)
68
69 Oy 3 SerSeGluGluGluGluValIleGlyCysHisSerValAspGluTrpIlyGluGluPhe 22
70 ||||||| ||||||| ||||||| ||||||| ||| |||
71 Db 69 TCATCCGAGGAGGACAAAGTGTTCGGCTCCACAAAGGTTGACGAATGGACGAATACTTC 128
72 23 GlnIlyGlyValAspSerIlySlySleuValValIleAspPheTrnAlaSerTrpCysGly 42

```

```

Db      129 AAGAAAGCGCTTGAGCTAGAAACCTGCTGCTCATTTTACTGCTTTCATGCTGCGGS 188
Qy      43 ProcysarphPheIlealProIleuAlaGlumetalalysLysThrProHisValIle 62
Db      189 CTTTGGCGCTTTTATTTGCCCCCAATTTCTTGCTGACATTTCTTAAGAAGATGCCCATGTTATA 248
Qy      63 PheLeuLysValaspValaspGluLeuLysThrValAla-GluGluPheLysValGluAl 82
Db      249 TTCCTCAAGGTTGATGTGATGAACCTGAGACTGTTTCAGCGGGAATGGAGTGTGGAGGC 308
Qy      82 aMetProThPheValPheLeuLysGluGlyLysGluValGluArgLeuValGluAlaAr 102
Db      309 AATGCCAACTTTTGTCTTTCATTTAAAGATGGAAAGAGATGGACAGCTTGTGCTGCCAA 368
Qy      102 gLysGluLysGluLeuAlaThrValGluLysHisGlyValA-----IleThrAla 118
Db      369 GAAGAAGAGATTTGCACGACACCATAGTGAAGCATGCTGCTCTGCTACTGTCAGCTGCT 426

RESULT 8
US-08-454-876-103
; Sequence 103, Application US/08454876
; Patient No. 5804693
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Melus, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Speirson, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Ukens, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Sherica C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; City: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,876
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566

```

```

; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-454-876-103

Alignment Scores:
Pred. No.: 7,81e-57 Length: 653
Score: 473.50 Matches: 90
Percent Similarity: 88.33% Conservative: 16
Best Local Similarity: 75.00% Mismatches: 10
Query Match: 78.01% Indels: 4
DB: 1 Gaps: 1

US-09-786-715-4 (1-118) x US-08-454-876-103 (1-653)
Qy      3 SerSerGluGluGlyGlnValIleGlyCysHisSerValaspGluThrPlyGluGlnPhe 22
Db      69 TCATCCGAGAGGAGGACAGTTCGCTGCCACAGGTGAGGAATGGAACGAGTACTTC 128
Qy      23 GlnLysGlyValaspSerLysLysLeuValValIleAspPheThrAlaSerTPCySGly 42
Db      129 AAGAAAGCGCTTGAGCTAGAAACCTGCTGCTCATTTTACTGCTTTCATGCTGCGGS 188
Qy      43 ProcysarphPheIlealProIleuAlaGlumetalalysLysThrProHisValIle 62
Db      189 CTTTGGCGCTTTTATTTGCCCCCAATTTCTTGCTGACATTTCTTAAGAAGATGCCCATGTTATA 248
Qy      63 PheLeuLysValaspValaspGluLeuLysThrValAla-GluGluPheLysValGluAl 82
Db      249 TTCCTCAAGGTTGATGTGATGAACCTGAGACTGTTTCAGCGGGAATGGAGTGTGGAGGC 308

```

Qy 82 ametProthrpheValPheLeuLysGluGlyValGluArgLeuValGlyAlaAr 102
 Db 309 AATGCCAACTTTGCTTCATTAAGATGAAAGAACTGACAGAGTTGTCGCCAA 368
 Qy 102 glysGluGluLeuGlnAlaThrValGluLysHisGlyAla-----IleThrAla 118
 Db 369 GAAAGAGAGTTGACGACGACCAATAGTGAGACATGCTCTGCTACTGTCACGTCT 426

RESULT 9

US-08-457-364-103
 Sequence 103, Application US/08457364
 Patent No. 5847258
 GENERAL INFORMATION:
 APPLICANT: Ryals, John A.
 APPLICANT: Alexander, Danny C.
 APPLICANT: Beck, James J.
 APPLICANT: Duesting, John H.
 APPLICANT: Friedrich, Leslie B.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Harms, Christian
 APPLICANT: Meins, Jr., Frederick
 APPLICANT: Montoya, Alice
 APPLICANT: Moyer, Mary B.
 APPLICANT: Neuhaus, Jean-Marc
 APPLICANT: Payne, George B.
 APPLICANT: Sperison, Christoph
 APPLICANT: Stinson, Jeffrey R.
 APPLICANT: Uknes, Scott J.
 APPLICANT: Ward, Eric R.
 APPLICANT: Williams, Shericea C.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/457,364
 FILING DATE: 31-MAY-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/181,271
 FILING DATE: 13-JAN-94
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,847
 FILING DATE: 6-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/632,441
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT 1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8614
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 653 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-457-364-103

Alignment Scores:
 Pred. No.: 7,81e-57 Length: 653
 Score: 473.50 Matches: 90
 Percent Similarity: 88.33% Conservative: 16
 Best Local Similarity: 75.00% Mismatches: 10
 Query Match: 78.01% Indels: 4
 DB: 2 Gaps: 1

US-09-786-715-4 (1-118) x US-08-457-364-103 (1-653)

Qy 3 SerSergLugluGluValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
 Db 69 TCATCCGAGGAGGCGACAGAGTTGCGCTGCCACAGAGTTGAGAGATGAGACGAGTCTTC 128
 Qy 23 GlnLysGlyValAspSerLysLysLeuValIleAspPheThrAlaSerTrpCysGly 42
 Db 129 AAGAAAGCGGTGACACAGAACTGCTGCTGCTGCTTACTGCTTCACTGCGCGS 188
 Qy 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysThrProHisValIle 62
 Db 189 CCTTGCCTTTATTTGCCCCCAATCTTCTGACATGCTTAAGAGATGCCCATGTTTATA 248
 Qy 63 PheLeuLysValAspValAspGluLeuLysThrValAla-GluGluPheLysValGluAl 82
 Db 249 TTCCCTCAAGGTTGATGTGATGAGTGAAGACTGTTTCAGGGGGAATGAGAGTGAGAGC 308
 Qy 82 ametProthrpheValPheLeuLysGluGlyValGluArgLeuValGlyAlaAr 102
 Db 309 AATGCCAACTTTGCTTCATTAAGATGAAAGAACTGACAGAGTTGTCGCCAA 368
 Qy 102 glysGluGluLeuGlnAlaThrValGluLysHisGlyAla-----IleThrAla 118
 Db 369 GAAAGAGAGTTGACGACGACCAATAGTGAGACATGCTCTGCTACTGTCACGTCT 426
 RESULT 10
 US-08-456-262-103
 Sequence 103, Application US/08456262

Patent No. 5851766
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesling, John H.
APPLICANT: Friedlich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Spertson, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,262
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PL/CSC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-456-262-103
Alignment Scores:
Pred. No.: 7.81e-57 Length: 653
Score: 473.50 Matches: 90
Percent Similarity: 88.33% Conservative: 16
Best Local Similarity: 75.00% Mismatches: 10
Query Match: 78.01% Indels: 4
Gaps: 1
US-09-786-715-4 (1-118) x US-08-456-262-103 (1-653)
QY 3 SerSerGluGluGluGluValIleGlyCysHisSerValaspGluTrpGluGluPhe 22
Db 69 TCATCCGAGGAGGACAGGTTCGCTGCACAGGTTGAGAAAGAGAGTACTTC 128
QY 23 GlnLysGlyValaspSerLysLysLeuValValIleaspPheThrAlaSerPcysGly 42
Db 129 AAGAAAGCGCTTAGACTAGAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 188
QY 43 ProCysArgPheIleAlaPheIleAlaGluMetAlaLysLysThrProHisValIle 62
Db 189 CCTTGGCGTTTATTGGCCCAATTCCTGACATTGCTAAGAAAGATGCCCATGTTATA 248
QY 63 PheLeuLysValaspValaspGluLeuLysThrValAla-GluGluPheLysValGluAla 82
Db 249 TTCCTCAAGGTTGATGTTGATGAGACTGATGACGGGAATGAGTGTGAGGCC 308
QY 82 ametrProThrPheValPheLeuLysGluGluValGluValGluValGluValGluVal 102
Db 309 AATGCCACATTTGCTCTCATTTAAAGATGGAAGAAGATGACAGATGTTGTGTGCCAA 368
QY 102 GlyGluGluGluGluAlaThrValGluLysHisGlyAla-----IleThrAla 118
Db 369 GAAAGAGAGGATTCACAGACCATAGTAAGACATGCTGCTGCTACTACTGCT 426
RESULT 11
US-08-456-240-103
Sequence 103, Application US/08456240
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesling, John H.
APPLICANT: Friedlich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice

APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESS: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,240
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott

REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CSC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-456-240-103
Alignment Scores:
Pred. No.: 7,81e-57 Length: 653
Score: 473.50 Matches: 90
Percent Similarity: 88.33% Conservative: 16
Best Local Similarity: 75.00% Mismatches: 10
Query Match: 78.01% Indels: 4
Gaps: 1
US-09-786-715-4 (1-118) x US-08-456-240-103 (1-653)
QY 3 SerSerGluGluGlyGlnValIleGlyCysHisSerValAspGluTrpLysGluInPhe 22
DB 69 TCATCCGAGGAGGACCAAGTGTTCGTCGCCCAAGGTTGAGCAATGAGACGATCTTC 128
QY 23 GlnLysGlyValAspSerLysLysLeuValIleAspPheThAlaSerTrpCysGly 42
DB 129 AAGAAAGCGCTTGACACTAAGAAACTGGTGGTGCATTTTACGCTTCAAGCGCCG 188
QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThProHisValIle 62
DB 189 CCTTCGCTTTATTTGCCCAATCTCTGTCATTCGTAAGAAAGATGCGCATGTATA 248
QY 63 PheLeuLysValAspValAspGluLeuLysThrValAla-GluGluPheLysValGluAl 82
DB 249 TTCCTCAAGGTGATGATGATGACTGAAGACTGTTTCACGCGGAATGGATGTGAGGCG 308
QY 82 AmePProThrPheValPheLeuLysGluGlyLysGluValGluArgLeuValGlyAla 102
DB 309 AATGCCACTTTTGTCTTCATTAAGATGAAAGAAAGTGCACAGATGTTGTGCGCCAA 368
QY 102 GlySGluGluLeuGlnAlaThrValGluLysHisGlyAla-----IleThrAla 118
DB 369 GAAAGAGGAGTTGCACGACAGACCATGATGAGAGCATGCTCCTGCTACTGTCATGCT 426
RESULT 12
US-08-456-736-103
Sequence 103, Application US/08455736
Patent No. 5880328
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
NUMBER OF SEQUENCES: 106

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: CIBA-GEIGY Corporation
;; STREET: 7 Skyline Drive
;; City: Hawthorne
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10532
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/455,736
;; FILING DATE: 31-MAY-1995
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/181,271
;; FILING DATE: 13-JAN-1994
;; APPLICATION NUMBER: US 08/093,301
;; FILING DATE: 16-JUL-1993
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/937,197
;; FILING DATE: 6-NOV-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/678,378
;; FILING DATE: 1-APR-1991
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/305,566
;; FILING DATE: 6-FEB-1989
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/165,667
;; FILING DATE: 8-MAR-1988
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/042,847
;; FILING DATE: 6-APR-1993
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/632,441
;; FILING DATE: 21-DEC-1990
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/425,504
;; FILING DATE: 20-OCT-1989
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/848,506
;; FILING DATE: 6-MAR-1992
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/768,122
;; FILING DATE: 27-SEP-1991
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/580,431
;; FILING DATE: 7-SEP-1990
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/368,672
;; FILING DATE: 20-JUN-1989
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/329,018
;; FILING DATE: 24-MAR-1989
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/045,957
;; FILING DATE: 12-APR-1993
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Elmer, James Scott
;; REGISTRATION NUMBER: 36,129
;; REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919)541-8614
;; TELEFAX: (919)541-8689
;; INFORMATION FOR SEQ ID NO: 103:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 653 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear

;; MOLECULE TYPE: DNA (genomic)
;; US-08-455-736-103
;;
;; Alignment Scores:
;; Pred. No.: 7,81e-57 Length: 653
;; Score: 473.50 Matches: 90
;; Percent Similarity: 88.33% Conservative: 16
;; Best Local Similarity: 75.00% Mismatches: 10
;; Query Match: 78.01% Indels: 4
;; DB: 2 Gaps: 1
;;
;; US-09-786-715-4 (1-118) x US-08-455-736-103 (1-653)
;;
QY 3 SerSerGluGluGlnGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
Db 69 TCATCCGAGGAGGAGACAGTTCGGCTGCCACAGGTTGAGGAAATGACGAGTACTTC 128
QY 23 GlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
Db 129 AAGAAAGCGCTTGACTAAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 188
QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysTrpProHisValIle 62
Db 189 CTTGCCGCTTTATTTGCCCAATCTTCTGACATTCCTAAGAAAGATGCCCATGTATA 248
QY 63 PheLeuLysValAspValAspGluLeuLysThrValAla-GluGluPheLysValGluAl 82
Db 249 TTCCTCAAGCTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 308
QY 82 aMetProThrPheValPheLeuLysGluGlnValGluValGluValGluValGluVal 102
Db 309 AATGCCAAGCTTTGCTCTCTTAAGATGGAAGAAGTGGACAGATTTGTGTGCCAA 368
QY 102 GlyGluGluLeuGluAlaThrValGluLysHisGlyAla-----IleThrAla 118
Db 369 GAAAGAGAGTTCACAGACACATATGAAAGCATGCTGCTGCTGCTGCTGCTGCTGCT 426
;;
RESULT 13
;; US-08-971-217-103
;; Sequence 103, Application US/08971217
;; Patent No. 5942652
;;
;; GENERAL INFORMATION:
;; APPLICANT: Ryals, John A.
;; APPLICANT: Harms, Christian
;; APPLICANT: Friedlich, Leslie
;; APPLICANT: Beck, James
;; APPLICANT: Uknes, Scott
;; APPLICANT: Ward, Eric
;; TITLE OF INVENTION: INDUCIBLE HERBICIDE RESISTANCE
;; NUMBER OF SEQUENCES: 111
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 594262artis Corporation
;; STREET: 3054 Cornwalis Road, P.O. Box 12257
;; City: Research Triangle Park
;; STATE: NC
;; COUNTRY: USA
;; ZIP: 27709
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/971,217
;; FILING DATE:
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/457,364
;; FILING DATE: 31-MAY-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/181,271
;; FILING DATE: 13-JAN-1994
;; PRIOR APPLICATION DATA:

```

      : APPLICATION NUMBER: US 08/093,301
      : FILING DATE: 16-JUL-1993
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 07/937,197
      : FILING DATE: 6-NOV-1992
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 07/678,378
      : FILING DATE: 1-APR-1991
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 07/305,566
      : FILING DATE: 6-FEB-1989
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 07/165,667
      : FILING DATE: 8-MAR-1988
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 08/042,847
      : FILING DATE: 6-APR-1993
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 07/632,441
      : FILING DATE: 21-DEC-1990
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 07/425,504
      : FILING DATE: 20-OCT-1989
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 07/848,506
      : FILING DATE: 6-MAR-1992
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 07/768,122
      : FILING DATE: 27-SEP-1991
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 07/580,431
      : FILING DATE: 7-SEP-1990
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 07/368,672
      : FILING DATE: 20-JUN-1989
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 07/329,018
      : FILING DATE: 24-MAR-1989
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: US 08/045,957
      : FILING DATE: 12-APR-1993
      : ATTORNEY/AGENT INFORMATION:
      : NAME: Meigs, J. Timothy
      : REGISTRATION NUMBER: 38,241
      : REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV5/CONT
      : TELECOMMUNICATION INFORMATION:
      : TELEPHONE: (919)541-8587
      : TELEFAX: (919)541-8689
      : INFORMATION FOR SEQ ID NO: 103:
      : SEQUENCE CHARACTERISTICS:
      : LENGTH: 653 base pairs
      : TYPE: nucleic acid
      : STRANDEDNESS: single
      : TOPOLOGY: linear
      : MOLECULE TYPE: DNA (genomic)
      : US-08-971-217-103

Alignment Scores:
Pred. NO.:          7,81e-57           Length:        653
Score:             473.50              Matches:         90
Percent Similarity: 88.33%              Conservative:    16
Best Local Similarity: 75.00%            Mismatches:     10
Query Match:       78.01%               Indels:         4
DB:                2                   Gaps:          1

US-09-786-715-4 (1-118) x US-08-971-217-103 (1-653)
OY      3   SerSerGluGluGlyGlnValIleGlyCysHisSerValAspLutTrpYsgLugInPhe 22
Db      69   TCAATCCGAGAGGACAAAGTGTTCGGCTCCCAACAAGTTGAGGAATGGAACGAGTACTTC 128
OY      23   GlnYsgLYValAspSerLYsLYsLeuValValIIeAspPherhrrAlasertTPCYsgLY 42
      : ::::::::::::::::::::

```

```

Db      129  ANAAGAGCGCTTGACGACTAGAAAGAACTGGTGGTGCATTTTACTGCTCATGGTGGGS 188
QY      43    ProCysArgPheIleAlaProIleuAlaGluMetAlaLysLysThrProHisValIle 62
        |||||||
Db      189  CTTTGGCCGTTTATTATTCGCCCAATCTTGCTGTCATGCTTAAGAAGATGCCCATGTTATA 248
QY      63    PheLeuLysValAspValAspIleuLysThrValAla-GluGluPheLysValGluAla 82
        |||||||
Db      249  TTCCTCAAGCTTGATCTTGATGAACTGGAAGACTGTTTCAGCGGGAATGGAAGTGTGGAGGC 308
QY      82  aMetProThrPheValPheLeuLysGluGlyLysGluValGluArgLeuValGluAlaAr 102
        |||||||
Db      309  AATGCCAACTTTTGCTCTTCAATTAAAGATGGAAGAAAGAAAGTGCACAGATGTTGTCGCCAA 368
QY      102  gLysGluGluLeuGluAlaThrValGluLysHisGlyValA-----IleThrAla 118
        |||||||
Db      369  GAAAGAGGAGTTTGACACAGACCAATGATGTAAGACATGCTGCTCTGCTACTGTCACTGCT 426
RESULT 14
US-09-350-600-103
; Sequence 103, Application US/09350600
; Patent No. 6262342
GENERAL INFORMATION:
APPLICANT: Meins, Frederick
APPLICANT: Shushl, Hideaki
APPLICANT: Wenzler, Herman
APPLICANT: Hofsteenge, Jan
APPLICANT: Ryals, John
APPLICANT: Spertsen, Christoph
TITLE OF INVENTION: DNA SEQUENCES ENCODING POLYPEPTIDES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6262342artis Corporation
STREET: 3054 Cornwallis Road, P.O. Box 12257
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,600
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/971,217
FILING DATE: 14-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,364
FILING DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,271
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847

```

```

: FILING DATE: 6-APR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/632,441
: FILING DATE: 21-DEC-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/425,504
: FILING DATE: 20-OCT-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/848,506
: FILING DATE: 6-MAR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/768,122
: FILING DATE: 27-SEP-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/580,431
: FILING DATE: 7-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/368,672
: FILING DATE: 20-JUN-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/329,018
: FILING DATE: 24-MAR-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/381,443
: FILING DATE: 18-JUL-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/353,312
: FILING DATE: 17-MAY-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/226,303
: FILING DATE: 29-JUL-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/045,957
: FILING DATE: 12-APR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: S-198250
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919)541-8587
: TELEFAX: (919)541-8689
: INFORMATION FOR SEQ ID NO: 103:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 653 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-09-350-600-103

Alignment Scores:
Pred. No.: 7.81e-57 Length: 653
Score: 473.50 Matches: 90
Percent Similarity: 88.33% Conservative: 16
Best Local Similarity: 75.00% Mismatches: 10
Query Match: 78.01% Indels: 4
DB: 3 Gaps: 1

US-09-786-715-4 (1-118) x US-09-350-600-103 (1-653)
QY 3 SerSerIuGlugluGlnValIleGlyCySHisSerValAspGIuTrpLysGluGlnPhe 22
Db 69 TCATCCAGAGGAGGACAAAGTTCGCTGCCACAAAGTTGAGGAATGGAAGCAAGTACTTCT 128
QY 23 GlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
Db 129 AAGAAAGCGCTTGAGACTAAGAACTGCTGCTCATTTTACTGCTTCTCATGCTGCGGS 188
QY 43 ProCysArpPheIleAlaProIleLeuAlaGluMetAlaLysLysTrpProHisValIle 62
Db 189 CTTTGCCGTTTATTGCCCAATCTCTGTCGACATCTCTAAGAAAGATGCCCAATGTATA 248
QY 63 PheLeuLysValAspValAspGluLeuLysThrValAla-GluGluPheLysValGluAl 82
```

```

Db 249 TTCCTCAAGGTTGATGTGAGACTGAAGCTTTTCAGCGGGAATGAGTGTGAGGC 308
QY 82 aMetProThrPheValPheLeuLysGluGlyValGluIleArgLeuValGlyAlaAr 102
Db 309 AATGCCAAGCTTTCTCTTCATTAAGATGAAAGAAAGTGAACAGATGTTGTGTCGCA 368
QY 102 gLysGluGluLeuGlnAlaThrValGluLysHisGlyAla-----IleThrAla 118
Db 369 GAAGAGAGAGTTGCAGCAGACATATGAAAGCATGCTCTCTCTACTGTACTGCT 426

RESULT 15
US-09-540-014-1
: Sequence 1, Application US/09540014
: Patent No.: 6380372
: GENERAL INFORMATION:
: APPLICANT: Cho, Myeong-Je
: APPLICANT: Del Val, Greg
: APPLICANT: Calliau, Maxime
: APPLICANT: Lemaux, Peggy G.
: APPLICANT: Buchanan, Bob B.
: TITLE OF INVENTION: Barley Gene for Thioredoxin and
: TITLE OF INVENTION: NADP-Thioredoxin Reductase
: FILE REFERENCE: 2001-0701.30
: CURRENT APPLICATION NUMBER: US/09/540,014
: CURRENT FILING DATE: 2000-03-31
: PRIOR APPLICATION NUMBER: US 60/127,198
: PRIOR FILING DATE: 1999-03-31
: PRIOR APPLICATION NUMBER: US 60/169,162
: PRIOR FILING DATE: 1999-12-06
: PRIOR APPLICATION NUMBER: US 60/177,740
: PRIOR FILING DATE: 2000-01-21
: PRIOR APPLICATION NUMBER: US 60/177,739
: PRIOR FILING DATE: 2000-01-21
: NUMBER OF SEQ ID NOS: 51
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 369
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: barley thioredoxin h cDNA
: US-09-540-014-1

Alignment Scores:
Pred. No.: 1.21e-41 Length: 369
Score: 362.00 Matches: 67
Percent Similarity: 77.19% Conservative: 21
Best Local Similarity: 58.77% Mismatches: 26
Query Match: 59.64% Indels: 0
DB: 4 Gaps: 0

US-09-786-715-4 (1-118) x US-09-540-014-1 (1-369)
QY 2 AlaSerSerGIuGlugluGlnValIleGlyCySHisSerValAspGIuTrpLysGluGln 21
Db 19 GCGGCGGCGAGTGGCGGCGGAGTGCATCTCGTCCACAGCCGTGAGCAGTGCACCATG 78
QY 22 PheGlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCys 41
Db 79 ATCGAGAGAGGCCAACACCGCCCAAGAGCTGCTGATTCATCTCATCTGCATCTGCTGC 138
QY 42 GlyProCysArpPheIleAlaProIleLeuAlaGluMetAlaLysLysTrpProHisVal 61
Db 139 GACACATGCGCGCATCATGCGCTCCAGTTTTCGCTGATCTCGCGCAAGAAAGTCCCAATG 198
QY 62 IlePheLeuLysValAspValAspGluLeuLysThrValAlaGluGluPheLysValGlu 81
Db 199 GTTTCCTCAAGGTCGAGCGTGGAGAACTGAAGCCATTCTCTGAGCAATTCAGTGCAG 258
QY 82 AlaMetProThrPheValPheLeuLysGluGlyValGluIleArgLeuValGlyAla 101
Db 259 GCCATGCCAACGTTCTCTCTCATATGAAAGAAAGAGAGCTCAAGGACAGGTTGTGAGACT 318
```


QY 102 ArgLysGluLueGlnAlaThrValGluLysHisGlyAla 115
|||||
Db 319 ATCAAGAGAGAACTGACCGCCCAAGGTTGGGCTTTCACGCGCG 360

Search completed: August 17, 2003, 21:45:13
Job time : 49.7308 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 19:25:47 ; Search time 137.545 Seconds

(without alignments) 1919.938 Million cell updates/sec

Title: US-09-786-715-4

Perfect score: 607

Sequence: 1 MASSEGGVICHSDYEMKE.....YGARKEELQATYERKALTA 118

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1504479 seqs, 1118970152 residues

Total number of hits satisfying chosen parameters: 3008958

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlp
-MODEL=framer_p2n.model -DEV=xlp
-O=/cgn2_1/USPTO_spool/US09786715/runatc_11082003_150515_6129/app_query.fasta_1.1052
-DB=Published_Applications_NA -OFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -SPART=1 -END=1 -MATRIX=blosum62
-FRAN=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MILEN=0
-MAXLEN=2000000000 -USER=US09786715_@CGN_1.1.560_@runatc_11082003_150515_6129
-NCPU=6 -ICPU=3 -NO_MAP -LARGEDEVY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published_Applications_NA.*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	437	72.0	392	10	US-09-878-574-104	Sequence 104, App

2	434	71.5	402	10	US-09-878-574-3723	Sequence 3723, Ap
3	430	70.8	390	10	US-09-878-574-1462	Sequence 1462, Ap
4	420	69.2	388	9	US-09-897-898-10	Sequence 10, Appl
5	419	69.0	345	10	US-09-938-842A-163	Sequence 163, App
6	419	69.0	3129	9	US-09-897-898-5	Sequence 5, Appl1
7	419	69.0	3888	9	US-09-897-898-7	Sequence 7, Appl1
8	390	64.3	540	12	US-10-349-782-12	Sequence 12, Appl
9	389	64.1	357	10	US-09-938-842A-1736	Sequence 1736, Ap
10	389	64.1	357	14	US-10-322-362-1	Sequence 1, Appl1
11	374.5	61.7	360	10	US-09-938-842A-164	Sequence 164, App
12	362	59.6	369	12	US-10-194-885-8	Sequence 8, Appl
13	361	59.6	369	12	US-10-091-841-1	Sequence 1, Appl1
14	361	59.5	659	12	US-10-349-782-9	Sequence 9, Appl1
15	358	59.0	382	12	US-10-091-841-3	Sequence 3, Appl1
16	358	59.0	393	12	US-10-091-841-5	Sequence 5, Appl1
17	324	53.4	260	10	US-09-878-574-12941	Sequence 12941, A
18	324	53.4	270	10	US-09-878-574-13445	Sequence 13445, A
19	321	52.9	277	10	US-09-878-574-8135	Sequence 8135, Ap
20	309	50.9	370	10	US-09-878-574-3169	Sequence 3169, Ap
21	305	50.2	268	10	US-09-878-574-5995	Sequence 5995, Ap
22	301	49.6	272	10	US-09-878-574-12181	Sequence 12181, A
23	295	48.6	402	10	US-09-938-842A-225	Sequence 225, App
24	295	48.6	613	9	US-09-770-146-855	Sequence 855, App
25	286	47.1	250	9	US-09-923-876-1288	Sequence 1288, Ap
26	285	47.0	267	10	US-09-878-574-13137	Sequence 13137, A
27	279	46.0	297	12	US-10-349-782-11	Sequence 11, Appl
28	279	46.0	456	10	US-09-924-035A-677	Sequence 677, App
29	256	42.2	390	10	US-09-938-842A-2688	Sequence 2688, Ap
30	249	41.0	413	14	US-10-102-524-1396	Sequence 1396, Ap
31	249	41.0	418	10	US-09-796-692-3641	Sequence 3641, Ap
32	249	41.0	418	14	US-10-040-862-3641	Sequence 3641, Ap
33	249	41.0	464	10	US-09-998-598-1059	Sequence 1059, Ap
34	249	41.0	479	11	US-09-535-459-1145	Sequence 1145, Ap
35	249	41.0	536	14	US-10-066-543-65	Sequence 65, Appl
36	249	41.0	540	10	US-09-920-300A-1247	Sequence 1247, Ap
37	249	41.0	547	13	US-10-033-528-1247	Sequence 1247, Ap
38	249	41.0	557	10	US-09-884-441-88	Sequence 88, Appl
39	249	41.0	557	11	US-09-907-969-88	Sequence 88, Appl
40	249	41.0	557	14	US-10-198-053-88	Sequence 88, Appl
41	249	41.0	557	14	US-09-535-459-1139	Sequence 1139, Ap
42	249	41.0	570	11	US-09-535-459-1149	Sequence 1149, Ap
43	249	41.0	594	10	US-09-884-441-87	Sequence 87, Appl
44	249	41.0	594	11	US-09-907-969-87	Sequence 87, Appl
45	249	41.0	594	14	US-10-198-053-87	Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-09-878-574-104
Sequence 104, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: BYRUM, Joseph R.
APPLICANT: Ia Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
PRIORITY FILING DATE: 2001-12-21
PRIORITY APPLICATION NUMBER: 09/333,535
PRIORITY FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 104
LENGTH: 392
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-056-01-B1-B3
US-09-878-574-104
Alignment Scores: 1.82e-53 Length: 392
Pred. No.:

Score: 437.00 Matches: 77
Percent Similarity: 86.09% Conservative: 22
Best Local Similarity: 66.96% Mismatches: 16
Query Match: 71.99% Indels: 0
DB: 10 Gaps: 0

US-09-786-715-4 (1-118) x US-09-878-574-104 (1-392)

QY 4 SerGlugluGluValIleGlyCysHisSerValAspGluTrpLysGluGluPheGln 23
DB 9 GCTGAAGAGGCTCAGGTTGCGCGTCACACCTTATGCTGGAACACACCTGCGAG 68
QY 24 LysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGlyPro 43
DB 69 AATGGAAGAGCTCCCAAAATTTGATTTGCTGATTTTACTGCTTCTGCTGCTGCTGCA 128
QY 44 CysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIlePhe 63
DB 129 TGGCGTTTATGCGCCAGTTCTGCGAGAGATTGCTGAGCATCTCTCAAGTATCTTC 188
QY 64 LeuLysValAspValAspGluLeuLysThrValAlaGluLuphLysValGluAlaMet 83
DB 189 CTCAGGTGATGTGATGATGAGTACGCGCTGCTGAGATTTCCATTGAGCGCATG 248
QY 84 ProThrPheValPheLeuLysGluGlyLysGluValAlaLuphLeuValGlyAlaArgLys 103
DB 249 CCAACCTTCCTCTTCTTGAAGAAGATGCGCAAGATCTGATGATGATGATGATGATG 308
QY 104 GluGluLeuGluAlaThrValGluLysHisGlyValIlePheAla 118
DB 309 GAGAGCTGCACTCACCATTGACCAAGCATGATCTGCTGCTGCT 353

RESULT 2

US-09-878-574-3723
; Sequence 3723, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(13401)B
; CURRENT APPLICATION NUMBER: US/09/878, 574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333, 535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3723
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-006-Q1-B1-F8
US-09-878-574-3723

Alignment Scores:

Pred. No.: 5.1e-53 Length: 402
Score: 434.00 Matches: 79
Percent Similarity: 86.61% Conservative: 18
Best Local Similarity: 70.54% Mismatches: 15
Query Match: 71.50% Indels: 0
DB: 10 Gaps: 0

US-09-786-715-4 (1-118) x US-09-878-574-3723 (1-402)

QY 4 SerGlugluGluValIleGlyCysHisSerValAspGluTrpLysGluGluPheGln 23
DB 46 GCGGAAGAGGCAAGATGATGCTGCTCAGCGCTAAGTGAAGCAACATCTCAG 105
QY 24 LysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGlyPro 43
DB 106 AAGGAGAGAGCTCCCAAGAAATTTGATTTGCTGATTTTACTGCTTCTTCTGCTGCTGCA 165

QY 44 CysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIlePhe 63
DB 166 TGGCGTTTATGCGCCAGTTCTGCGAGAGATTGCTGAAGAAAGTTGCGGAATGTCACCTTC 225
QY 64 LeuLysValAspValAspGluLeuLysThrValAlaGluLuphLysValGluAlaMet 83
DB 226 CTCACGCTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 285
QY 84 ProThrPheValPheLeuLysGluGlyLysGluValAlaLuphLeuValGlyAlaArgLys 103
DB 286 CCAACCTTCCTCTTCTTGAAGAAGATGCGCAAGCTGTCGCAAGATTGCTGCTGCTGCTG 345
QY 104 GluGluLeuGluAlaThrValGluLysHisGlyVal 115
DB 346 GAGAGCTGCAATGACCTTACCGCAGACATGCGCA 381

RESULT 3

US-09-878-574-1462
; Sequence 1462, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(13401)B
; CURRENT APPLICATION NUMBER: US/09/878, 574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333, 535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1462
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-037-Q1-B1-F11
US-09-878-574-1462

Alignment Scores:

Pred. No.: 1.83e-52 Length: 390
Score: 430.00 Matches: 77
Percent Similarity: 88.18% Conservative: 20
Best Local Similarity: 70.00% Mismatches: 13
Query Match: 70.84% Indels: 0
DB: 10 Gaps: 0

US-09-786-715-4 (1-118) x US-09-878-574-1462 (1-390)

QY 1 MetAlaSerSerGluGluGluValIleGlyCysHisSerValAspGluTrpLysGlu 20
DB 57 ATGCGTGAAGTGAAGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATG 116
QY 21 GluPheGluLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrp 40
DB 117 CAACTCCAGATGCAAGAAAGATGCAAGAAAGATGCAAGATGCAAGATGCAAGATGCAAG 176
QY 41 CysGlyProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHis 60
DB 177 TGTGCTCATGCGCTTTATGCGCGCTTCTTCAAGATGCAAGAAAGAACTCCGGA 236
QY 61 ValIlePheLeuLysValAspValAspGluLeuLysThrValAlaGluLuphLysVal 80
DB 237 TTGATCTTCTCAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 296
QY 81 GluAlaMetProThrPheValPheLeuLysGluGlyLysGluValAlaLuphLeuValGly 100
DB 297 GAGGCCATGCAACCTTCCTTCTTGAAGAAGATGCGAATGCGCAAGGATGCGTGGT 356
QY 101 AlaArgLysGluGluLeuGluAlaThrVal 110
DB 357 GCTAGTAGGATGACCTTCAAGCCACCATA 386

RESULT 4
US-09-897-898-10
; Sequence 10, Application US/09897898
; Patent No. US20020037303A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.
; APPLICANT: VAN ROOIJEN, GJIS
; APPLICANT: BOOTHE, JOSEPH
; APPLICANT: GOLL, JANIS
; APPLICANT: MOLONEY, MAURICE M.
; APPLICANT: DALMIA, BIPIN K.
; TITLE OF INVENTION: THIOREDOLIN AND THIOREDOLIN REDUCTASE CONTAINING OIL
; FILE REFERENCE: 034547/0104
; CURRENT APPLICATION NUMBER: US/09/897, 898
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/577,147
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 09/448,600
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 09/084,777
; PRIOR FILING DATE: 1998-05-27
; PRIOR APPLICATION NUMBER: 60/047,753
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: 60/047,779
; PRIOR FILING DATE: 1997-05-28
; PRIOR APPLICATION NUMBER: 60/075,863
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/075,864
; PRIOR FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 3888
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1555)..(2250)
; NAME/KEY: CDS
; LOCATION: (2491)..(2655)
; OTHER INFORMATION: Description of Unknown Organism: Phaseolin
; OTHER INFORMATION: promoter-Tyrh oleosin-phaseolin terminator
US-09-897-898-10
Alignment Scores:
Pred. No.: 1,32e-49 Length: 3888
Score: 420.00 Matches: 74
Percent Similarity: 85.96% Conservative: 24
Best Local Similarity: 64.91% Mismatches: 16
Query Match: 69.19% Indels: 0
Gaps: 0
US-09-786-715-4 (1-118) x US-09-897-898-10 (1-3888)
QY 3 SerSerGluGluGluGluValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
Db 1558 GCTTCGGAAGAGCAAGTGTATCGCTCCACACCGCTTGAGACATGAGACGAGCTT 1617
QY 23 GlnLysGlyValAspSerLysLysLeuValIleAspPheThrAlaSerTrpCysGly 42
Db 1618 CAGAAAGCTAAATGATCCAAACTCTGTGTGTGTTGATTTCACGCGCTTCTGTGTGTA 1677
QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
Db 1678 CCATGTCGTTTCATGCTCCATCTTCTGCTGATTGGCTAAGAACTTCCTAACGCTT 1737
QY 63 PheLeuLysValAspValAspLysLeuLysThrValAlaGluGluPheLysValGluAla 82
Db 1738 TTCCTCAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1797
QY 83 MetProThrPheValPheLeuLysGluGluValGluAlaGluArgLeuValGluAlaArg 102

Db 1798 ATGCCACCTTCATGTTTGTGAGGAAGGAGGAGATTTGGACAAAGTTGTGGACCAAG 1857
QY 103 LysGluGluLeuGlnAlaThrValGluLysHisGlyAlaIle 116
Db 1858 AAGATGAGCTTCAGTCACTACATTCGCAACACCTTGCTATG 1899
RESULT 5
US-09-938-842A-163
; Sequence 163, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 163
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-163
Alignment Scores:
Pred. No.: 5,85e-51 Length: 345
Score: 419.00 Matches: 73
Percent Similarity: 86.49% Conservative: 23
Best Local Similarity: 65.77% Mismatches: 15
Query Match: 69.03% Indels: 0
Gaps: 0
US-09-786-715-4 (1-118) x US-09-938-842A-163 (1-345)
QY 3 SerSerGluGluGluGluValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
Db 4 GCTTCGGAAGAGCAAGTGTATCGCTCCACACCGCTTGAGACATGAGACGAGCTT 63
QY 23 GlnLysGlyValAspSerLysLysLeuValIleAspPheThrAlaSerTrpCysGly 42
Db 64 CAGAAAGCTAAATGATCCAAACTCTGTGTGTGTTGATTTCACGCGCTTCTGTGTGTA 123
QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
Db 124 CCATGTCGTTTCATGCTCCATCTTCTGCTGATTGGCTAAGAACTTCCTAACGCTT 183
QY 63 PheLeuLysValAspValAspLysLeuLysThrValAlaGluGluPheLysValGluAla 82
Db 184 TTCCTCAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
QY 83 MetProThrPheValPheLeuLysGluGluValGluAlaGluArgLeuValGluAlaArg 102
Db 244 ATGCCACCTTCATGTTTGTGAGGAAGGAGGAGATTTTGACAAAGTTGTGGACCAAG 303
QY 103 LysGluGluLeuGlnAlaThrValGluLysHis 113
Db 304 AAGATGAGCTTCAGTCACTACATTCGCAACACCTTGCTATG 336
RESULT 6
US-09-897-898-5
; Sequence 5, Application US/09897898
; Patent No. US20020037303A1
; GENERAL INFORMATION:
; APPLICANT: DECKERS, HARM M.

Db 2617 AAGATGAGCTTCAGTCTACATTCGCAACAC 2649

RESULT 8

US-10-349-782-12

Sequence 12, Application US/10349782

Publication No. US20030143618A1

GENERAL INFORMATION:

APPLICANT: Yves Hatzfield

APPLICANT: Valerie Marie-No. US20030143618A1lle Frankard

APPLICANT: Anne-Marie Droual

TITLE OF INVENTION: Method for easy cloning and selection of chimeric DNA molecules

FILE REFERENCE: 1187-15

CURRENT APPLICATION NUMBER: US/10/349,782

CURRENT FILING DATE: 2003-01-23

PRIOR APPLICATION NUMBER: EP 02075373.7

PRIOR FILING DATE: 2002-01-23

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 12

LENGTH: 540

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Modified thioredoxin of Oryza sativa in vector pDONR201

US-10-349-782-12

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
1,62e-46	540	71	21	24	0

Score: 390.00

Percent Similarity: 79.31%

Best Local Similarity: 61.25%

Query Match: 12 Gaps: 0

US-09-786-715-4 (1-118) x US-10-349-782-12 (1-540)

QY 3 SerSeGIUGlUGlVAlIeGIcYSHISserValASpGIurTrpLysGIuInPhe 22

Db 61 GCCCGGAGAGGAGAGTCTGATCGCTGCCACACAGAGAGAGTTCAGCCCGGAG 120

QY 23 GlnYsGIuValASpSerLysLysLysLysLysLysLysLysLysLysLysLysLys 42

Db 121 ACCAAGGCCAGAGAGGCGCGCAAGTGTGATATGACTGCTGCTGCTGCTGCTG 180

QY 43 ProCYSArgPheIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 62

Db 181 CCGTGGCGCTTCATCGCCCGAGTTCGCTGATATGAGTTCGCTGCTGCTGCTG 240

QY 63 PheLeuLysValASpValASpLysLysLysLysLysLysLysLysLysLysLysLys 82

Db 241 TTCCTGAGAGTTCATGCTGATGAGTTCGAGAGAGTTCGAGAGAGTTCGAGAG 300

QY 83 MetProThrPheValPheLeuLysGIuValASpLysLysLysLysLysLysLysLys 102

Db 301 ATGCCGACCTTCCTATTCATCAAGAGTGTGCTGAGAGTGTGCTGAGAGTGTG 360

QY 103 LysGIuLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 118

Db 361 AAGGATGACCTTCAGAGACATCTGAGAGACGCTGCTGCTGCTGCTGCTGCT 408

RESULT 9

US-09-938-842A-1736

Sequence 1736, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kieps, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

FILE REFERENCE: SCDP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

US-09-938-842A-1736

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 1736

LENGTH: 357

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-1736

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
1.25e-46	357	70	21	22	0

Score: 389.00

Percent Similarity: 80.53%

Best Local Similarity: 61.95%

Query Match: 10 Gaps: 0

US-09-786-715-4 (1-118) x US-09-938-842A-1736 (1-357)

QY 6 GlnGIuValIleGIcYSHISserValASpGIurTrpLysGIuInPheGlnLysGly 25

Db 10 GAGAGAGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 69

QY 26 ValASpSerLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 45

Db 70 AACGATTCACAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 129

QY 46 PheIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 65

Db 130 TTCATTGACCCCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 189

QY 66 ValASpValASpLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 85

Db 190 GTGATGTTGACCAATTCAGACACTGTTGCTGAGAGATTTAAAGTTAGGCAATGCC 249

QY 86 PheValPheLeuLysGIuValASpLysLysLysLysLysLysLysLysLysLysLys 105

Db 250 TTATCTTCATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 309

QY 106 LeuGlnAlaThrValGlnLysLysLysLysLysLysLysLysLysLysLysLys 118

Db 310 ATCATTGCCAATCTCGAAGAGACAGACAGATGTTGCT 348

RESULT 10

US-10-323-362-1

Sequence 1, Application US/10323362

Publication No. US20030113786A1

GENERAL INFORMATION:

APPLICANT: Kurnik, Betsy

APPLICANT: Davis, Keith

APPLICANT: Zayed, Adel

APPLICANT: Ascenzi, Robert

APPLICANT: Harper, Angel

APPLICANT: Boyes, Douglas

APPLICANT: Mulpur, Rao

APPLICANT: Hoffman, Neil

APPLICANT: Kjemtrup, Susanne

APPLICANT: Moessner, Jeffrey

APPLICANT: Goriach, John

APPLICANT: Hamilton, Carol

TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF INHIBITORS OF THIOREDOXIN EX

FILE REFERENCE: 213305

CURRENT APPLICATION NUMBER: US/10/323,362

CURRENT FILING DATE: 2002-12-18

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

```

; LENGTH: 357
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-323-362-1

Alignment Scores:
Pred. No.: 1.25e-46 Length: 357
Score: 389.00 Matches: 70
Percent Similarity: 80.53% Conservative: 21
Best Local Similarity: 61.95% Mismatches: 22
Query Match: 64.09% Indels: 0
DB: 14 Gaps: 0

US-09-786-715-4 (1-118) x US-10-323-362-1 (1-357)
Qy 6 GluGluGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPheGlnLysGly 25
Db 10 GAAGAGAGAGTTATCGCTGCCACACCGTTGAGATTGGACCGAGAACCTCAAGCCGCC 69
Qy 26 ValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGlyProCysArg 45
Db 70 AACGATCCAGAAACGATGTGTGATACCTCACTGCAACATGCTGCCACCTGCCGT 129
Qy 46 PheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIlePheLeuLys 65
Db 130 TTCATTGCACCCGCTTGTCTGACTGACTGACCAAGACACTGCACTGATGCTCTTCAAG 189
Qy 66 ValAspValAspGluLeuLysThrValAlaGluGlnPheLysValAlaMetProThr 85
Db 190 GTGATGTTGACGATTCGATGACACTGTTCTGAGAGTTAAAGTTCAGGCAATGCCAAG 249
Qy 86 PheValPheLeuLysGluGlyLysGluValGluArgLeuValAlaArgLysGluGlu 105
Db 250 TTTATCTTCATGAAGAAGAGAGATCAAGAGACTGTGGTGGCTGCTAAAGAAAGAA 309
Qy 106 LeuGlnAlaThrValGluLysHisGlyAlaIleThrAla 118
Db 310 ATCATGTGCATCTCGAGAGACAGACAGACTGTGTCT 348

RESULT 11
US-09-938-842A-164
; Sequence 164, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kieps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; PRIOR APPLICATION NUMBER: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 164
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-164

Alignment Scores:
Pred. No.: 1.53e-44 Length: 360
Score: 374.50 Matches: 72
Percent Similarity: 76.72% Conservative: 17
Best Local Similarity: 62.07% Mismatches: 26
Query Match: 61.70% Indels: 1
DB: 10 Gaps: 1

```

```

US-09-786-715-4 (1-118) x US-09-938-842A-164 (1-360)
Qy 3 SerSerGluGluGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
Db 4 GCGGAGAGAGAGGATGATGATGTTGTGTACACGAGACGATGATGATGATGATGAT 63
Qy 23 GlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
Db 64 GATTAAGCCAAAGATTCACACAGCTGATGATGATGATGATGATGATGATGATGATGAT 123
Qy 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLys---ThrProHisVal 61
Db 124 CCATGCCCATGATGCTCCCAATTTTCAACGATTTGGCAAGAGATTTCATGATCAAGTCC 183
Qy 62 IlePheLeuLysValAspValAspGluLeuLysThrValAlaGluGlnPheLysValGlu 81
Db 184 ATCTTCTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 243
Qy 82 AlaMetProThrPheValPheLeuLysGluGlyLysGluValGluArgLeuValAla 101
Db 244 GCATGCCACACTTGTGTCTTATTAACCGCGCAAGTGTGATGATGATGATGATGATGAT 303
Qy 102 ArgLysGluGluLeuGlnAlaThrValGluLysHisGlyAlaIleThr 117
Db 304 AATTAAGAGAGATCTTCAAGCGCAAAATAGTGAACATAGTGTGATCA 351

RESULT 12
US-10-194-885-8
; Sequence 8, Application US/10194885
; Publication No. US20030135878A1
; GENERAL INFORMATION:
; APPLICANT: Wong, J. H.
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH ELEVATED
; FILE REFERENCE: 416272000800
; CURRENT APPLICATION NUMBER: US/10/194, 885
; PRIOR APPLICATION NUMBER: 2002-07-12
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 09/538, 864
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/126,736
; PRIOR FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Barley
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(369)
US-10-194-885-8

Alignment Scores:
Pred. No.: 9.92e-43 Length: 369
Score: 362.00 Matches: 67
Percent Similarity: 77.19% Conservative: 21
Best Local Similarity: 58.77% Mismatches: 26
Query Match: 59.64% Indels: 0
DB: 12 Gaps: 0

US-09-786-715-4 (1-118) x US-10-194-885-8 (1-369)
Qy 2 AlaSerSerGluGluGlnValIleGlyCysHisSerValAspGluTrpLysGluGln 21
Db 19 GCGGCGGAGATGCGGCGGAGAGTATCTCGTCCACAGACCTGAGACAGTGGACATGACG 78
Qy 22 PheGlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCys 41

```



```
Db 79 ATCGAGGAGGCCAACACCGCCCAAGAGCTGGTGGTATTGACTTCACTGCATCATGGTGC 138
QY 42 GlyProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisVal 61
Db 139 GGACCATGCCGATCATGGCTCCAGCTTTTCGCTGATCTCGCCCAAGAACTTCCCAAAATGCT 198
QY 62 IlePheLeuLysValAspValAspLeuLysThrValAlaGluGluPheLysValGlu 81
Db 199 GTTTCCTCAAGGTGACGTGGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 258
QY 82 AlaMetProThrPheValPheLeuLysGluLysGluValGluLysHisGlyAla 101
Db 259 GCCATGCCAAGCTTCTCTTCAATGAAGGAAGGAGACGTCAAGGACAGAGGTTGTCGGAGCT 318
QY 102 ArgLysGluGluLeuGluAlaThrValGluLysHisGlyAla 115
Db 319 ATCAAGGAGGAAGTCAAGCCCAAGGTTGGGCTTCAAGCGGCG 360

RESULT 13
US-10-091-841-1
; Sequence 1, Application US/10091841
; Publication No. US20030150010A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresdoxin and
; FILE OF INVENTION: NADP-Thioresdoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/10/091,841
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: barley thioresdoxin h cDNA
US-10-091-841-1

Alignment Scores:
Pred. No.: 9,92e-43 Length: 369
Score: 362.00 Matches: 67
Percent Similarity: 77.19% Conservativeness: 21
Best Local Similarity: 58.77% Mismatches: 26
Query Match: 59.64% Indels: 0
DB: 12 Gaps: 0

US-09-786-715-4 (1-118) x US-10-091-841-1 (1-369)
QY 2 AlaSerSerGluGluGlyGlnValIleGlyCysHisSerValAspGluTrpLysGluGln 21
Db 19 GCGGCGGAGTGGCGGCGGAGTGTATCTCGTCCACAGCTGGAGCAGTGCATGACG 78
QY 22 PheGlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCys 41
Db 79 ATCGAGGAGGCCAACACCGCCCAAGAGCTGGTGGTATTGACTTCACTGCATCATGGTGC 138
QY 42 GlyProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisVal 61
```

```
Db 139 GSACCATGCCGATCATGGCTCCAGTTCCTTCGCTGATCTCGCCCAAGAGTTCCCAAAATGCT 198
QY 62 IlePheLeuLysValAspValAspLeuLysThrValAlaGluGluPheLysValGlu 81
Db 199 GTTTCCTCAAGGTGACGTGGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 258
QY 82 AlaMetProThrPheValPheLeuLysGluLysGluValGluLysHisGlyAla 101
Db 259 GCCATGCCAAGCTTCTCTTCAATGAAGGAAGGAGACGTCAAGGACAGAGGTTGTCGGAGCT 318
QY 102 ArgLysGluGluLeuGluAlaThrValGluLysHisGlyAla 115
Db 319 ATCAAGGAGGAAGTCAAGCCCAAGGTTGGGCTTCAAGCGGCG 360

RESULT 14
US-10-349-782-9
; Sequence 9, Application US/10349782
; Publication No. US20030143618A1
; GENERAL INFORMATION:
; APPLICANT: Valerie Marie-No. US20030143618A1111111 Frankard
; APPLICANT: Anne-Marie Droual
; TITLE OF INVENTION: Method for easy cloning and selection of chimeric DNA molecule
; FILE REFERENCE: 1187-15
; CURRENT APPLICATION NUMBER: US/10/349,782
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: EP 02075373.7
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 659
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Thioresdoxin of Oryza sativa in vector pDONR201
US-10-349-782-9

Alignment Scores:
Pred. No.: 3,15e-42 Length: 659
Score: 361.00 Matches: 70
Percent Similarity: 78.45% Conservativeness: 21
Best Local Similarity: 60.34% Mismatches: 25
Query Match: 59.47% Indels: 1
DB: 12 Gaps: 0

US-09-786-715-4 (1-118) x US-10-349-782-9 (1-659)
QY 3 SerSerGluGluGlyGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
Db 133 GCGGCGGAGGAGGAGTGTATCTCGTCCACACAGGAGTTCGACGCCCATG 192
QY 23 GlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
Db 193 ACCAAGGCCAAGGAGGCGGCAAGTGTGTCATATTTGACTTCACTGCTTCTTGGTGTGC 252
QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
Db 253 CCTTCCGCTTCATCGCCCGGAGTGTGCTGAATACGCGCAAAAGTTCCCTGGTGTGTC 312
QY 63 PheLeuLysValAspValAspLeuLysThrValAlaGluGluPheLysValGluAla 82
Db 313 TTCTTGAAGTGTGATGTTGATGAGTGAAGGAGTGTGTTGAAGAGTACATATTCGAGGCA 372
QY 83 MetProThrPheValPheLeuLysGluLysGluValGluLysHisGlyAlaArg 102
Db 373 ATGCGGACCTTCCTATT-ATCAAGGATGCTGCTGAGGTGACAAAGTCTGTTGGCCGAGG 431
QY 103 LysGluGluLeuGluAlaThrValGluLysHisGlyAlaIleThrAla 118
Db 432 AAGGATGACCTCCAGAACCATCATGTAAGCAGCTCGGTGCGCTGCTGCT 479
```

RESULT 15

US-10-091-841-3
 : Sequence 3, Application US/10091841
 : Publication No. US20030150010A1
 : GENERAL INFORMATION:
 : APPLICANT: Cho, Myeong-Je
 : APPLICANT: Del Val, Greg
 : APPLICANT: Caillau, Maxime
 : APPLICANT: Lemaux, Peggy G.
 : APPLICANT: Buchanan, Bob B.
 : TITLE OF INVENTION: Barley Gene for Thioresdoxin and
 : TITLE OF INVENTION: NADP-Thioresdoxin Reductase
 : FILE REFERENCE: 2001-0701.30
 : CURRENT APPLICATION NUMBER: US/10/091,841
 : PRIORITY FILING DATE: 2002-03-05
 : PRIOR APPLICATION NUMBER: 09/540,014
 : PRIOR FILING DATE: 2000-03-31
 : PRIOR APPLICATION NUMBER: US 60/127,198
 : PRIOR FILING DATE: 1999-03-31
 : PRIOR APPLICATION NUMBER: US 60/169,162
 : PRIOR FILING DATE: 1999-12-06
 : PRIOR APPLICATION NUMBER: US 60/177,740
 : PRIOR FILING DATE: 2000-01-21
 : PRIOR APPLICATION NUMBER: US 60/177,739
 : PRIOR FILING DATE: 2000-01-21
 : NUMBER OF SEQ ID NOS: 51
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 3
 : LENGTH: 382
 : TYPE: DNA
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: wheat thioresdoxin h cDNA
 US-10-091-841-3

Alignment Scores:
 Pred. No.: 3-91e-42 Length: 382
 Score: 358.00 Matches: 67
 Percent Similarity: 77.06% Conservative: 17
 Best Local Similarity: 61.47% Mismatches: 25
 Query Match: 58.98% Indels: 0
 DB: 12 Gaps: 0

US-09-786-715-4 (1-118) x US-10-091-841-3 (1-382)

QY	7	GlyGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPheGlnLysGlyVal	26
DB	52	GGGGAGGTGATCTCCGTCACAGCCCTGGAGCAGTGGACCATCGAGGAGGCCAAC	111
QY	27	AspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGlyProCysArgPhe	46
DB	112	GGCGCCCAAGAGCTGCTGTTGATGACTTCACCTGTCATGCTGGCGGACCATGCCGCATT	171
QY	47	IleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIlePheLeuLysVal	66
DB	172	ATGGCTCCAAATTTTCGCTGATCTCGCAAGAAGTTCCACAGTCTGTTTCTCTCAAGGTC	231
QY	67	AspValAspGluLeuLysThrValAlaGluGluPheLysValGluAlaMetProThrPhe	86
DB	232	GAGGTTGATGAACTGAAGCCCATGCTGAGCAATTCAGGTCGAGGCCATGCCACCTTC	291
QY	87	ValPheLeuLysGluGlyLysGluValGluArgLeuValIleAlaArgLysGluGluLeu	106
DB	292	CTGTTTCATGAAGAGGAGATGTCAGAGGACAGGGTTGTCGAGCTATCAAGGAGGAATG	351
QY	107	GlnAlaThrValGluLysHisGlyAla	115
DB	352	ACGACCAAGGTTGGGCTACACGCGCC	378

Search completed: August 17, 2003, 23:43:49
 Job time : 140.545 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 17, 2003, 19:20:27 ; Search time 1595.81 Seconds
(without alignments)
1797.162 Million cell updates/sec

Title: US-09-786-715-4
Perfect score: 607
Sequence: 1 MASSREGVICHSYDVENKE.....VGARKEELQATVERKGATTA 118

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 segs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_plus.model -DEV=xlp
-Q=/cgn2.1/USPTO_POOL/US09786715/runat_11082003_150514_6048/app_query.fasta_1.1052
-DB=EST -QFMT=fastap -SUFFIX=1st -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR.SCORE=Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=tbl -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09786715_66CN_1_1_7834_@runat_11082003_150514_6048 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEDEV -NEG.SCOES=0 -WAIT -DSPHLOG=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vr1:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	527	86.8	441	12	BM173053
2	512	84.3	433	12	BM173035
3	492	81.1	452	14	CA524170
4	480	80.7	455	9	A1773303
5	480	80.7	477	9	AM041395
6	480	80.7	505	9	AM094525
7	480	80.7	541	9	A1776110
8	480	80.7	546	9	AM038924
9	480	80.7	547	9	AM038141
10	480	80.7	552	9	AM625331
11	480	80.7	564	9	A1775760
12	480	80.7	567	9	AM037831
13	480	80.7	570	12	BI208736
14	480	80.7	573	9	A1778940
15	480	80.7	573	9	A1781827
16	480	80.7	581	9	AM096472
17	480	80.7	594	9	AM650009
18	480	80.7	615	9	AM621673
19	480	80.7	617	9	A1780240
20	480	80.7	619	12	BI210657
21	480	80.7	622	12	BI206688
22	480	80.7	623	9	AM625957
23	480	80.7	694	9	AM040001
24	480	80.7	694	9	AM040011
25	480	80.7	731	12	BI203833
26	489	80.6	455	10	BF050482
27	485	79.9	565	9	AM040195
28	485	79.9	565	9	AM040201
29	485	79.9	624	13	BQ507669
30	485	79.9	628	10	BG598337
31	485	79.9	648	13	BQ507668
32	482	79.4	382	9	AM038564
33	481	79.2	480	9	AM626018
34	477	78.6	574	12	BM063442
35	477	78.6	575	10	BG130196
36	477	78.6	637	12	BM065241
37	476	78.4	494	12	BM878771
38	476	78.4	579	13	BM692317
39	470	77.4	564	13	BU692458
40	470	77.4	590	12	BG890096
41	466	76.8	508	9	AM625037
42	459	75.6	548	14	CA896876
43	459	75.6	555	14	CA901892
44	459	75.6	601	14	CA896877
45	458	75.5	464	9	AL386021

ALIGNMENTS

RESULT 1
BM173053
LOCUS
DEFINITION
LOCUS
900407 Avicennia marina leaf cDNA library Avicennia marina cDNA
clone Am900407 5' similar to thioredoxin (X58527) of Nicotiana
tabacum, mRNA sequence.
ACCESSION
BM173053
VERSION
BM173053.1 GI:17312616
KEYWORDS
EST.
SOURCE
Avicennia marina
ORGANISM
Avicennia marina
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; Lamiales; Acanthaceae; Acanthaceae Incertae
 sedis; Avicennia.
 1 (bases 1 to 441)
 REFERENCE
 TITLE
 AUTHORS
 JOURNAL
 COMMENT

Parami, M., Mehta, P., Sivaprakash, K.R. and Parida, A.
 Expressed sequence tags from the mangrove species Avicennia marina
 Unpublished
 Contact: Parami M / Parida A
 Department of Plant Molecular Biology
 M. S. Swaminathan Research Foundation
 111 Cross Street, Taramani Institutional Area, Chennai 600 113,
 India
 Tel: 91-44-2351319
 Fax: 91-44-2351319
 Email: mangrovegenes@msrf.res.in
 BLAST search in BLASTX (Non-redundant) using default parameters as
 on November 6th 2001
 Seq primer: M13 Reverse.

FEATURES
 SOURCE

Location/Qualifiers
 1..441
 /organism="Avicennia marina"
 /mol_type="mRNA"
 /strain="Pichavaram"
 /db_xref="taxon:82927"
 /clone="Am900407"
 /sex="Hermaphrodite"
 /tissue_type="leaf"
 /dev_stage="1 year old plant"
 /clone_1id="Avicennia marina leaf cDNA library"
 /note="A one-year-old plant from the natural mangrove
 habitat in Pichavaram, Tamil Nadu, India was collected
 and brought to the M.S.Swaminathan Research Foundation.
 The whole plant was treated with the nutrient solution
 supplemented with 500 mM NaCl for 48 hours. Poly(A⁺)mRNA
 from the leaf tissue was purified and cDNA was prepared
 using Superscript Lambda System (Life Technologies, Cat.
 No. 19643-014). The cDNAs were size fractionated over
 SizeSep-400 spun column (Amersham-Pharmacia Biotech Cat
 No. 27-5105-01) and cloned in 5'Sal I - 3' Not I of
 pSPORT1 (Life Technologies Cat. No. 15383-011). The ESTs
 were sequenced from the 5' end using M13/pUC18 reverse
 primer in an Automated Sequencer (ABI3130, Applied
 Biosystems) and submitted after editing to remove the
 vector and adapter sequences. BLAST search in BLASTX
 (Non-redundant) was carried out on 7th August, 2000 using
 default parameters and the results reported under
 putative identification/comment"

BASE COUNT 106 a 89 c 122 g 124 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4,27e-60 Length: 441
 Score: 527.00 Matches: 97
 Percent Similarity: 93.16% Conservative: 12
 Best Local Similarity: 82.91% Mismatches: 8
 Query Match: 86.82% Indels: 0
 DB: 12 Gaps: 0

US-09-786-715-4 (1-118) x BM173053 (1-441)

Oy 2 AlaserserlugluglgnvalilleglyshiserValaspglutprlysglgn 21
 Db 3 GCTTCGCGAAGGGGTCAAGTATCGCTGCCACCTCCGGACGAGTGAAGACAT 62
 Oy 22 PheglinsgllyValaspserylsylsleuValailleasphethrAlasertpcys 41
 Db 63 TTCACAGAGGGCGTCAAGTCTAAAAACTGGTACTGTAGATTTCAGCGCTTCGTCTGC 122
 Oy 42 GlyProCysArghpellealaproileuAlaGluMetAlaLysLysThrProHisVal 61
 Db 123 GGACCTTCGCTTCATTCCTCCCAATTTGGCTGAGATCGCCAGAGAGTGGCCCTCAGTT 182
 Oy 62 IllephelneutysValaspValaspGluLeuLysThrValAlaGluLupheLysValGlu 81

Db 183 GTATTCCTGAAGTGCATGTTGATGAGCTTAAGACTGTGCTACTGATTCAGATTGAG 242
 Oy 82 AlametprothrphevalpheleulysglulysgluValaGluArgleuValGlyAla 101
 Db 243 GCTATGCTTACTCTTCTTCTTCACAAAGAGAAAGAAATGACAGCTTGTGGTGC 302
 Oy 102 ArglysglugluLeuGlnAlaThrValGluLysHsglyAlaIerhAla 118
 Db 303 AAGAGAGAGATCTGTGCGCCAGATCACCAACATGTTACCCCGTGGCT 353

RESULT 2
 BM173035

LOCUS
 DEFINITION
 900389 Avicennia marina leaf cDNA library Avicennia marina cDNA
 clone Am900389 5' similar to thiorodoxin (X58527) of Nicotiana
 tabacum, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BM173035 433 bp mRNA linear EST 04-DEC-2001
 BM173035.1 GI:17312598
 EST.
 Avicennia marina
 Avicennia marina
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; Lamiales; Acanthaceae; Acanthaceae Incertae
 sedis; Avicennia.
 1 (bases 1 to 433)
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Parami, M., Mehta, P., Sivaprakash, K.R. and Parida, A.
 Expressed sequence tags from the mangrove species Avicennia marina
 Unpublished
 Contact: Parami M / Parida A
 Department of Plant Molecular Biology
 M. S. Swaminathan Research Foundation
 111 Cross Street, Taramani Institutional Area, Chennai 600 113,
 India
 Tel: 91-44-2351319
 Fax: 91-44-2351319
 Email: mangrovegenes@msrf.res.in
 BLAST search in BLASTX (Non-redundant) using default parameters as
 on November 6th 2001
 Seq primer: M13 Reverse.

FEATURES
 SOURCE

Location/Qualifiers
 1..433
 /organism="Avicennia marina"
 /mol_type="mRNA"
 /strain="Pichavaram"
 /db_xref="taxon:82927"
 /clone="Am900389"
 /sex="Hermaphrodite"
 /tissue_type="leaf"
 /dev_stage="1 year old plant"
 /clone_1id="Avicennia marina leaf cDNA library"
 /note="A one-year-old plant from the natural mangrove
 habitat in Pichavaram, Tamil Nadu, India was collected
 and brought to the M.S.Swaminathan Research Foundation.
 The whole plant was treated with the nutrient solution
 supplemented with 500 mM NaCl for 48 hours. Poly(A⁺)mRNA
 from the leaf tissue was purified and cDNA was prepared
 using Superscript Lambda System (Life Technologies, Cat.
 No. 19643-014). The cDNAs were size fractionated over
 SizeSep-400 spun column (Amersham-Pharmacia Biotech Cat
 No. 27-5105-01) and cloned in 5'Sal I 3' Not I of
 pSPORT1 (Life Technologies Cat. No. 15383-011). The ESTs
 were sequenced from the 5' end using M13/pUC18 reverse
 primer in an Automated Sequencer (ABI3130, Applied
 Biosystems) and submitted after editing to remove the
 vector and adapter sequences. BLAST search in BLASTX
 (Non-redundant) was carried out on 7th August, 2000 using
 default parameters and the results reported under
 putative identification/comment"

BASE COUNT 112 a 87 c 118 g 116 t
 ORIGIN
 Alignment Scores:

Pred. No.: 4.2e-58 Length: 433
 Score: 512.00 Matches: 96
 Percent Similarity: 94.74% Conservative: 12
 Best Local Similarity: 84.21% Mismatches: 5
 Query Match: 84.35% Indels: 1
 DB: 12 Gaps: 0

US-09-786-715-4 (1-118) x BM173035 (1-433)

OY 1 MetAlaSerSerGluGluGlyGlnValIleGly-CysHisSerValAspGluTrpLysGln 20
 DB 71 ATGCGCTTCGTCGAGAGAGGCTCAAGTATGATGCTCCAGCTCCGTGAGAGAGGAAGA 130
 OY 20 uGlnPheGlnValAspSerLysLysValValIleAspPheThrAlaSerTr 40
 DB 131 GCATTTCAGAAAGGCGCTGAGCTAAAGAGGAGTGTAGATTTTACGGCTTCGTG 190
 OY 40 PCysGlyProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProH 60
 DB 191 GTCGGACCTTCGCTTCATTCATTCATTTTGGCTGATGCCAGAGAGTCCGCTCA 250
 OY 60 SVAlIlePheLeuLysValAspValAspGluLeuLysThrValAlaGluGluPheLysVa 80
 DB 251 TGTGTATTCCGAGAGGTGATGTGATGAGCTTAAGACTGTGCTACTGAATTCAGAT 310
 OY 80 lGluAlaMetProThrPheValPheLeuLysGluLysGluValGluArgLeuValGln 100
 DB 311 TTAGGCTATGCTTACCTCTTGTCTCTCAAGAGAGGAAAGAAATGACAGCGCTTGTGG 370
 OY 100 yAlaArgLysGluGluLeuGlnAlaThrValGluLysHis 113
 DB 371 TGCCAGAGAGAGATCTCTGCGCCAGATCACCAACAT 410

RESULT 3
 CA524170 452 bp mRNA linear EST 15-NOV-2002
 LOCUS KS1203303 KS12 Capsicum annuum cDNA, mRNA sequence.
 DEFINITION CA524170
 ACCESSION CA524170
 VERSION CA524170.1 GI:25038242
 KEYWORDS EST.
 SOURCE Capsicum annuum
 ORGANISM Capsicum annuum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Asterids; Lamiales; Magnoliophyta; eudicotyledons; core eudicots; 1 (bases 1 to 452)
 REFERENCE Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pai,H.-S., Hur,C.-G. and Choi,D.
 AUTHORS Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
 TITLE Unpublished
 JOURNAL Contact: Doll Choi
 COMMENT Genome Research Center and National Center for Genome Information
 P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
 Tel: 82-42-860-4340
 Fax: 82-42-860-4309
 Email: doll@mail.krrib.re.kr
 Plate: 033 row: H column: 03.

FEATURES
 source 1..452
 Location/Qualifiers
 1..452
 /organism="Capsicum annuum"
 /mol_type="mRNA"
 /db_xref="taxon:4072"
 /clone_lib="KS12"

BASE COUNT 116 a 75 c 121 g 140 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.09e-55 Length: 452
 Score: 492.00 Matches: 90
 Percent Similarity: 92.79% Conservative: 13

Best Local Similarity: 81.08% Mismatches: 8
 Query Match: 81.05% Indels: 0
 DB: 14 Gaps: 0

US-09-786-715-4 (1-118) x CA524170 (1-452)

OY 3 SerSerGluGluGlyGlnValIleGlyCysHisSerValAspGluTrpLysGlnPhe 22
 DB 66 TCATCTGAAGAGAGACAAAGTTTGGCTTGCCACAGAGTGGAGAGTGAAGCACTTC 125
 OY 23 GlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
 DB 126 AAGAGAGGTGTGACACTAAGAAATGTGTGTGATTTTACCCATCTCTGTCGGT 185
 OY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
 DB 186 CCTTGGCGTTTATTCCCAATTCCTGATGACATGTCAAGAGATGCCCATGTGCANA 245
 OY 63 PheLeuLysValAspValAspGluLeuLysThrValAlaGluGluPheLysValGluAla 82
 DB 246 TTCCTCAAGCTTGATTTGTATGACTAAAGACTTTGCGAGAGAAATGGAATGTGAAGCT 305
 OY 83 MetProThrPheValPheLeuLysGluLysGluValGluArgLeuValGluAlaArg 102
 DB 306 ATGCCAACATTTGTCTCTCTTAAGATGCGAAGAGTGAATGAGTGTGTGTGTCAG 365
 OY 103 LysGluGluLeuGlnAlaThrValGluLysHis 113
 DB 366 AAGAGAGAGTTCGAGCAGCAGCATATCAAGAT 398

RESULT 4
 A1773303 455 bp mRNA linear EST 18-MAY-2001
 LOCUS EST254403 tomato resistant, Cornell Lycopersicon esculentum cDNA
 DEFINITION clone CLERE63, mRNA sequence.
 ACCESSION A1773303
 VERSION A1773303.1 GI:5271344
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 455)
 REFERENCE D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D., Giovannoni,J.J. and Martin,G.B.
 AUTHORS Generation of ESTs from Pseudomonas resistant tomato
 TITLE Unpublished
 JOURNAL Other_ESTS: TC1792
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.

FEATURES
 source 1..455
 Location/Qualifiers
 1..455
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultiivar="RI1-12 (35S::Pro in Rio Grande x Money Maker)"
 /db_xref="taxon:4081"
 /clone_lib="CLERE63"
 /tissue_type="leaf"
 /dev_stage="4-week old"
 /lab_host="SOLR"
 /clone_lib="tomato resistant, Cornell"
 /note="Vector: pBluescript SK(-), Site_1: EcoRI, Site_2: XhoI; CLER - Tomato Pseudomonas Resistant EST Library. Directionally cloned cDNAs inserted into pBluescript SK(-) at 5' end with EcoRI and 3' end with XhoI site."

BASE COUNT 114 a 78 c 125 g 138 t

/cultivar="Rio Grande Ptor"
/db_xref="taxon:4081"
/clone="CLET29E19"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="X11-blue MRF"
/clone_lib="tomato mixed elicitor, BTI"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; CLEF - inoculated with a variety of disease response
elicitors. Plants exposed to 2,6 dichloroisonicotinic
acid, BTH, jasmonic acid, ethylene, fenthion, ETX,
okadaic acid, or systemin prior to tissue harvest. EcoRI
site was destroyed during cloning."

BASE COUNT

123 a 82 c 136 g 164 t

ORIGIN

Alignment Scores:

Pred. No.: 4,496-55 Length: 505
Score: 490.00 Matches: 91
Percent Similarity: 89.66% Conservative: 13
Best Local Similarity: 78.458 Mismatches: 12
Query Match: 80.72% Indels: 0
DB: 9 Gaps: 0

US-09-786-715-4 (1-118) x AM094525 (1-505)

OY 3 SerSerGluGluGlyGlnValIleGlyCysHISserValAspGluTrpLysGluGlnPhe 22
|||||
DB 30 TCATCTGAGGAGGAGACAAAGTATCGGCTCCACAAAGTTGAGAGAGTGAGAGCAGCTC 89
23 GlnLysGlyValAspSerLysLysLeuValIleAspPheThrLaseTrpCysGly 42
|||||
DB 90 CAGAGAGGTGTGAGAGCAGCAAAAACCTGCTGGTGATTTACTCTTCCTGCTGGTGGT 149
43 ProCysArgPheIleAlaProIleuAlaGluMetAlaLysLysThrProHisValIle 62
|||||
DB 150 CCTTCCGCTTTTATTTATTCCTCCCAATTCCTTGACATGCTAAGAAATGCCCATGTTTANG 209
63 PheLeuLysValAspAlaAspGluLeuLysThrValAlaGluGluPheLysValGluAla 82
|||||
DB 210 TTCCTCAAGGTGATGTATGATGAACGAAAGATTGTCAGAGAGAAATGATGTGAGGCA 269
83 MetProThrPheValPheLeuLysGluGlyLysGluValAlaGluGluPheLysValGluAla 102
|||||
DB 270 ATGCCAATCTTTGTCTCTCATTAAGAGGTTAAAGAGTGAATGATGATGCTTGTGCTGCAT 329
OY 103 LysGluGluLeuGlnAlaThrValGluLysHisGlyAlaIleThrAla 118
|||||
DB 330 AAAGACGATGCTTCAGACCAATAGAGAGCATGCTGCTCTCTCT 377

RESULT 7

A1776110

LOCUS A1776110 541 bp mRNA linear EST 18-MAY-2001

DEFINITION EST57198 tomato resistant, Cornell Lycopersicon esculentum CDNA
clone CLEF1702, mRNA sequence.

ACCESSION

A1776110

VERSION A1776110.1 GI:5274139

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 541)
D'Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman,
Giovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudomonas resistant tomato
unpublished
Contact: CGI
Clemson University Genomics Institute
Clemson University

100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source
Location/Qualifiers
1. 541

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="RI-12 (35S::Pro in Rio Grande x Money Maker)"

/db_xref="taxon:4081"

/clone="CLEF1702"

/tissue_type="leaf"

/dev_stage="4-week old"

/lab_host="SOLR"

/clone_lib="tomato resistant, Cornell"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; CLEF - Tomato Pseudomonas Resistant EST Library.
directionally cloned cDNAs inserted into pBluescript SK(-)
at 5' end with EcoRI and 3' end with XhoI site."

BASE COUNT

129 a 84 c 142 g 186 t

ORIGIN

Alignment Scores:

Pred. No.: 4,926-55 Length: 541
Score: 490.00 Matches: 91
Percent Similarity: 89.66% Conservative: 13
Best Local Similarity: 78.458 Mismatches: 12
Query Match: 80.72% Indels: 0
DB: 9 Gaps: 0

US-09-786-715-4 (1-118) x A1776110 (1-541)

OY 3 SerSerGluGluGlyGlnValIleGlyCysHISserValAspGluTrpLysGluGlnPhe 22
|||||
DB 75 TCATCTGAGGAGGAGACAAAGTATCGGCTCCACAAAGTTGAGAGAGTGAGAGCAGCTC 134
23 GlnLysGlyValAspSerLysLysLeuValIleAspPheThrLaseTrpCysGly 42
|||||
DB 135 CAGAGAGGTGTGAGAGCAGCAAAAACCTGCTGGTGATTTACTCTTCCTGCTGGTGGT 194
43 ProCysArgPheIleAlaProIleuAlaGluMetAlaLysLysThrProHisValIle 62
|||||
DB 195 CCTTCCGCTTTTATTTATTCCTCCCAATTCCTTGACATGCTAAGAAATGCCCATGTTTANG 254
63 PheLeuLysValAspAlaAspGluLeuLysThrValAlaGluGluPheLysValGluAla 82
|||||
DB 255 TTCCTCAAGGTGATGTATGATGAACGAAAGATTGTCAGAGAGAAATGATGTGAGGCA 314
83 MetProThrPheValPheLeuLysGluGlyLysGluValAlaGluGluPheLysValGluAla 102
|||||
DB 315 ATGCCAATCTTTGTCTCTCATTAAGAGGTTAAAGAGTGAATGATGATGCTTGTGCTGCAT 374
OY 103 LysGluGluLeuGlnAlaThrValGluLysHisGlyAlaIleThrAla 118
|||||
DB 375 AAAGACGATGCTTCAGACCAATAGAGAGCATGCTGCTCTCTCT 422

RESULT 8

AM038924

LOCUS AM038924 546 bp mRNA linear EST 18-MAY-2001

DEFINITION EST280880 tomato mixed elicitor, BTI Lycopersicon esculentum CDNA
clone CLEF10G5, mRNA sequence.

ACCESSION

AM038924

VERSION AM038924.1 GI:5897678

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 546)
D'Ascenzo, M., He, X., Lyman, J., Holt, I.E., Liang, F., Upton, J.,
Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, M.,
Fraser, C.M., Venter, J.C., Martin, G.B., Tankley, S.D. and Giovannoni,
J.

TITLE Generation of ESTs from tomato leaf tissue
JOURNAL Unpublished
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source Location/Qualifiers
1..546
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande ProR"
/db_xref="taxon:4081"
/clone="cLET10G5"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="X11-Blue MRF"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLET - Inoculated with a variety of disease response
elicitors. Plants exposed to 2,6 dichloroisocortinic
acid, BTH, jasmonic acid, ethylene, fenthion, EIX,
okadaic acid, or systemin prior to tissue harvest. EcoRI
site was destroyed during cloning."

BASE COUNT 129 a 84 c 145 g 188 t

ORIGIN

Alignment Scores:
Pred. No.: 4.98e-55 Length: 546
Score: 490.00 Matches: 91
Percent Similarity: 89.66% Conservative: 13
Best Local Similarity: 78.45% Mismatches: 12
Query Match: 80.72% Indels: 0
DB: 9 Gaps: 0

US-09-786-715-4 (1-118) x AM038924 (1-546)

QY 3 SerSerGluGluGlnGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
|||||
Db 77 TCATCTGAGGAGACACAGATGATGGCTGCCACAGGTGAGAGTGGAGAGTGCACCTC 136
23 GlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
|||||
Db 137 CAGAGGGGTGGGACCAAAAACCTGGTGGTGGATTTACTGCTTCCTGGTGGCGT 196
43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysTrpProHisValIle 62
|||||
Db 197 CTTGGCCGTTTATGGCCCAATTCCTGGTGCATTCCTAAGAGATGCCCATGTTATG 256
63 PheLeuLysValAspValAspGluLeuLysThrValAlaGluGluPheLysValGluAla 82
|||||
Db 257 TTCTCTAAGGTGATGTGATGAGACTGAGAAAGTTTCAGAGATGGAATGTGAGGCA 316
QY 83 MetProThrPheValPheLeuLysGluGlyLysGluValGluArgLeuValGlyAlaArg 102
|||||
Db 317 ATGCCAAGCTTTGCTTCATTAAAGAGGTAAGAAAGTGGATGAGTGGTGGCCAAAT 376
QY 103 LysGluGluLeuGlnAlaThrValGluLysHisGlyAlaIleThrAla 118
|||||
Db 377 AAAGACGAGATTGCTTCAGACCATAGAGACATGTGCTCTCTGCT 424

RESULT 9
AM038141 547 bp mRNA linear EST 18-MAY-2001
LOCUS EST279798 tomato mixed elicitor, BRT Lycopersicon esculentum CDNA
DEFINITION clone cLET1N21, mRNA sequence.
ACCESSION AM038141
VERSION AM038141.1 GI:5896895
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

TITLE Generation of ESTs from tomato leaf tissue
JOURNAL Unpublished
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source Location/Qualifiers
1..547
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande ProR"
/db_xref="taxon:4081"
/clone="cLET1N21"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="X11-Blue MRF"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLET - Inoculated with a variety of disease response
elicitors. Plants exposed to 2,6 dichloroisocortinic
acid, BTH, jasmonic acid, ethylene, fenthion, EIX,
okadaic acid, or systemin prior to tissue harvest. EcoRI
site was destroyed during cloning."

BASE COUNT 129 a 84 c 146 g 188 t

ORIGIN

Alignment Scores:
Pred. No.: 4.99e-55 Length: 547
Score: 490.00 Matches: 91
Percent Similarity: 89.66% Conservative: 13
Best Local Similarity: 78.45% Mismatches: 12
Query Match: 80.72% Indels: 0
DB: 9 Gaps: 0

US-09-786-715-4 (1-118) x AM038141 (1-547)

QY 3 SerSerGluGluGlnGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
|||||
Db 77 TCATCTGAGGAGACACAGATGATGGCTGCCACAGGTGAGAGTGGAGAGTGCACCTC 136
23 GlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
|||||
Db 137 CAGAGGGGTGGGACCAAAAACCTGGTGGTGGATTTACTGCTTCCTGGTGGCGT 196
QY 43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysTrpProHisValIle 62
|||||
Db 197 CTTGGCCGTTTATGGCCCAATTCCTGGTGCATTCCTAAGAGATGCCCATGTTATG 256
63 PheLeuLysValAspValAspGluLeuLysThrValAlaGluGluPheLysValGluAla 82
|||||
Db 257 TTCTCTAAGGTGATGTGATGAGACTGAGAAAGTTTCAGAGATGGAATGTGAGGCA 316
QY 83 MetProThrPheValPheLeuLysGluGlyLysGluValGluArgLeuValGlyAlaArg 102
|||||
Db 317 ATGCCAAGCTTTGCTTCATTAAAGAGGTAAGAAAGTGGATGAGTGGTGGCCAAAT 376
QY 103 LysGluGluLeuGlnAlaThrValGluLysHisGlyAlaIleThrAla 118
|||||
Db 377 AAAGACGAGATTGCTTCAGACCATAGAGACATGTGCTCTCTGCT 424

RESULT 10
AM625331 552 bp mRNA linear EST 18-MAY-2001
LOCUS EST319154 tomato radicle, 5 d post-imbibition, Cornell University

Lycopersicon esculentum cDNA clone cLE212117 5', mRNA sequence.
AM625331
VERSION AM625331.1 GI:7338274
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 552)
REFERENCE van der Hoeven, R.S., Garvin, D., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Niernman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato radicle tissue (etiolated)
AUTHORS Unpublished
JOURNAL Contact: CUGI
COMMENT Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source
1..552
Location/Qualifiers
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLE212117"
/tissue_type="radicle"
/dev_stage="seedlings 5 days post-imbibition"
/clone_lib="tomato radicle, 5 d post-imbibition, Cornell University"
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; supplier: Tanksley; tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."
BASE COUNT 131 a 86 c 146 g 189 t
ORIGIN
Alignment Scores:
Pred. No.: 5,05e-55 Length: 552
Score: 490.00 Matches: 91
Percent Similarity: 89.66% Conservative: 13
Best Local Similarity: 78.45% Mismatches: 12
Query Match: 80.72% Indels: 0
Gaps: 0
US-09-786-715-4 (1-118) x AM625331 (1-552)
QY 3 SerSerGluGluGlnValIleGlyCysHisSerValAspGluTrpLysGluInphe 22
Db 78 TCATCTGAAGAGACAAAGTGAATCGGCTGCCAAGAGTTGAGAGCTGACGCTC 137
QY 23 GlnLysGluValAspSerLysLysLeuValIleAspPheThrAlaSerTrpCysGly 42
Db 138 CAGAAAGGTGTGAGAACCAAAAAGTGTGTGTGATTTACTGCTTCCGTGCGCT 197
QY 43 ProCysArgPheIleAlaProIleuAlaGluMetAlaLysLysThrProHisValIle 62
Db 198 CCTTCCTGTTTATTTGCCCCAATTTCTGCTGCAATTTGCTAAAGAAATGCCCATGTATANG 257
QY 63 PheLeuLysValAspValAspGluLeuLysThrValAlaGluLupheLysValGluAla 82
Db 258 TTCCTCAAGGTGATGATGATGACTGAGAAAGTTGCAGAGAAATGGAATGTGAGGCA 317
QY 83 MetProThrPheValPheLeuLysGluGluValAlaGluArgLeuValGlyAlaArg 102
Db 318 ATGCCAATTTTGTCTTCATTAAGAGGTTAAAGAGTGAAGGTTTGTGTCGCAAT 377
QY 103 LysGluGluLeuGlnAlaThrValAlaLysHisGlyAlaIleThrAla 118
Db 378 AAAGACGATGCTTCTCAGACCATAGAGAAAGCATGCTGCTGCTCCT 425
RESULT 11

A1775760
LOCUS A1775760 564 bp mRNA linear EST 18-MAY-2001
DEFINITION EST256860 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER16B23, mRNA sequence.
ACCESSION A1775760
VERSION A1775760.1 GI:5273801
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 564)
REFERENCE D'Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Niernman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B. Generation of ESTs from Pseudomonas resistant tomato
AUTHORS Unpublished
JOURNAL Contact: CUGI
COMMENT Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source
1..564
Location/Qualifiers
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="R11-12 (35S::Pto In Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="cLER16B23"
/tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
/clone_lib="tomato resistant, Cornell"
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; cLER: Tomato Pseudomonas Resistant EST Library. Directionally cloned cDNAs inserted into pBluescript SK(-) at 5' end with EcoRI and 3' end with XhoI site."
BASE COUNT 134 a 94 c 147 g 189 t
ORIGIN
Alignment Scores:
Pred. No.: 5.2e-55 Length: 564
Score: 490.00 Matches: 91
Percent Similarity: 89.66% Conservative: 13
Best Local Similarity: 78.45% Mismatches: 12
Query Match: 80.72% Indels: 0
Gaps: 0
US-09-786-715-4 (1-118) x A1775760 (1-564)
QY 3 SerSerGluGluGlnValIleGlyCysHisSerValAspGluTrpLysGluInphe 22
Db 21 TCATCTGAAGAGACAAAGTGAATCGGCTGCCAAGTTGAGAGGAGGAGTGACGCTC 80
QY 23 GlnLysGluValAspSerLysLysLeuValIleAspPheThrAlaSerTrpCysGly 42
Db 81 CAGAAAGGTGTGAGAACCAAAAAGTGTGTGTGATTTACTGCTTCCGTGCGCT 140
QY 43 ProCysArgPheIleAlaProIleuAlaGluMetAlaLysLysThrProHisValIle 62
Db 141 CCTTCCTGTTTATTTGCCCCAATTTCTGCTGCAATTTGCTAAAGAAATGCCCATGTATANG 200
QY 63 PheLeuLysValAspValAspGluLeuLysThrValAlaGluLupheLysValGluAla 82
Db 201 TTCCTCAAGGTGATGATGATGACTGAGAAAGTTGCAGAGAAATGGAATGTGAGGCA 260
QY 83 MetProThrPheValPheLeuLysGluGluValAlaGluArgLeuValGlyAlaArg 102
Db 261 ATGCCAATTTTGTCTTCATTAAGAGGTTAAAGAGTGAAGGTTTGTGTCGCAAT 320

QY 103 LysgluGlueGlnAlaThrValGluLysHisGlyAlaIleThrAla 118
 Db 321 AAGACGGATTGCTTCAGACCATAGAGAAAGCATGTGCTGCTCGCT 368
 RESULT 12
 AM037831
 LOCUS AM037831 567 bp mRNA linear EST 18-MAY-2001
 DEFINITION EST279460 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA
 clone CLET3L21, mRNA sequence.
 ACCESSION AM037831
 VERSION AM037831.1 GI:5896585
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 REFERENCE 1 (bases 1 to 567)
 D'Ascenzo, M., He, X., Lyman, J., Holt, I.E., Liang, F., Upton, J.,
 Rinning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W.,
 Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni,
 J.
 TITLE Generation of ESTs from tomato leaf tissue
 JOURNAL Unpublished
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.
 FEATURES
 source Location/Qualifiers
 1..567
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="Rio Grande Pcor"
 /db_xref="taxon:4081"
 /clone="CLET3L21"
 /tissue_type="leaf"
 /dev_stage="4-6 week old plants"
 /lab_host="XLI-Blue MRP"
 /clone_idb="tomato mixed elicitor, BTI"
 /note="Vector: pluescript SK(-); Site,1: EcoRI; Site,2:
 XhoI; CLET : Inoculated with a variety of disease response
 elicitors. Plants exposed to 2,6 dichloroisonicotinic
 acid, BTH, jasmonic acid, ethylene, fenthion, Eix,
 okadaic acid, or systemin prior to tissue harvest. EcoRI
 site was destroyed during cloning."
 BASE COUNT 136 a 87 c 149 g 194 t 1 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.24e-55 Length: 567
 Score: 490.00 Matches: 91
 Percent Similarity: 89.66% Conservative: 13
 Best Local Similarity: 78.45% Mismatches: 12
 Query Match: 80.72% Indels: 0
 Gaps: 0
 US-09-786-715-4 (1-118) x AM037831 (1-567)
 QY 3 SerSerGluGluGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
 Db 77 TCATCTGAGAGAGACAAAGTGCATCGCTGCCACAAAGTTCAGAGAGTGCACATC 136
 QY 23 GlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
 Db 137 CAGAGGGGTGTGGAGACCAAAAACCTGTGTGTGATTTTACTGCTTCGTGGTGGGT 196
 QY 43 ProCysArpPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
 Db 197 CTTTGGCGTTTATGTCGCCAATTCCTGTCGACATTCCTAAGAGATGCCCATGTTATG 256
 QY 63 PheLeuLysValAspValAspGluLeuLysThrValAlaGluLupPheLysValGluAla 82

Db 257 TTCCTCAAGGTTGATGTGATGATGAACTGACAGAGATGATGTCGAGGCA 316
 QY 83 MetProThrPheValPheLeuLysGluGlyLysGluValAlaGluArgLeuValAlaArg 102
 Db 317 ATGCCAAGCTTTGCTTCATTAAAGAGGTAAGAGAGGATGAGGTTGTGTGCCAAT 376
 QY 103 LysgluGlueGlnAlaThrValGluLysHisGlyAlaIleThrAla 118
 Db 377 AAGACGGATTGCTTCAGACCATAGAGAAAGCATGTGCTGCTCGCT 424
 RESULT 13
 BI208736 570 bp mRNA linear EST 11-JUL-2001
 LOCUS BI208736
 DEFINITION EST526776 cTOS Lycopersicon esculentum cDNA clone cTOS17P22 5' end,
 mRNA sequence.
 ACCESSION BI208736
 VERSION BI208736.1 GI:14686460
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 REFERENCE 1 (bases 1 to 570)
 van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utlterback, R.,
 Rinning, C. and Tanksley, S.
 TITLE Generation of ESTs from Tomato Suspension Cultures
 JOURNAL Unpublished
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 1 prime sequence.
 FEATURES
 source Location/Qualifiers
 1..570
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496, E6203"
 /db_xref="taxon:4081"
 /clone="cTOS17P22"
 /tissue_type="suspension cultures"
 /lab_host="SOLR"
 /clone_idb="cTOS"
 /note="Vector: pluescript SK(-); Site,1: EcoRI; Site,2:
 XhoI; Suspension cultures of L.esculentum E6203 were grown
 in Murashige and Skoog based medium, supplemented with 15%
 coconut milk (filter sterilized and added after
 autoclaving), 2% saccharose, and 1mg/ml 2,4D (pH5.8).
 Fresh medium was added every 7 days, and cultures were
 grown at 25 C, with 12hrs of light and continuous
 shaking."
 BASE COUNT 134 a 97 c 148 g 191 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.27e-55 Length: 570
 Score: 490.00 Matches: 91
 Percent Similarity: 89.66% Conservative: 13
 Best Local Similarity: 78.45% Mismatches: 12
 Query Match: 80.72% Indels: 0
 Gaps: 0
 US-09-786-715-4 (1-118) x BI208736 (1-570)
 QY 3 SerSerGluGluGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
 Db 16 TCATCTGAGAGAGACAAAGTGCATCGCTGCCACAAAGTTCAGAGAGTGCACATC 75
 QY 23 GlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
 Db 76 CAGAGGGGTGTGGAGACCAAAAACCTGTGTGTGATTTTACTGCTTCGTGGTGGGT 135

QY 43 ProCysArgPheIleAlaProIleLeuAlaIleValIleAspPheThrProHisValIle 62
|||||
Db 136 CCTGCGCGTTTATTTGCCCCCAATTCCTGTCACATTCGTAAGAAGATGCCCATGTATTAG 195
63 PheLeuLysValAspValAspIleLeuLysThrValAlaIleGluPheLysValGluAla 82
|||||
Db 196 TTCCTCAAGGTTGATGTTGATGACACTGAGAAAGTTGCAGAGAAATGGAATGTGGAGCA 255
QY 83 MetProThrPheValPheLeuLysGluLysGluValGluAlaGluValGluAlaGly 102
Db 256 ATGCCAAGCTTTGTCTCTCAATTAAGAGGGTTAAAGAGTGAATGAGGTGTGTGTGCCAAT 315
QY 103 LysGluGluLeuGlnAlaThrValAlaGluLysHisGlyAlaIleThrAla 118
Db 316 AAGAGCGATTCCTTCAGACCATAGAGAGCATGTGCTGCTCTCTCT 363

RESULT 14
A1778940 573 bp mRNA linear EST 18-MAY-2001
LOCUS EST259819 tomato susceptible, Cornell Lycopersicon esculentum cDNA
DEFINITION clone CLES6J23, mRNA sequence.
ACCESSION A1778940
VERSION A1778940.1 GI:5276981
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 573)
REFERENCE D'Ascenzo,M., He,X., Lyman,J.J., Matero,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
C.L., Nieman,M., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Giovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas susceptible tomato
UNPUBLISHED
JOURNAL Contact: CUGI
COMMENT Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source
1..573
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="RI1-13 (Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="CLES6J23"
/tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
/clone_1lb="tomato susceptible, Cornell"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; CLES - Tomato Pseudomonas Susceptible EST library.
directionally cloned cDNAs inserted into pBluescript SK(-
) at 5' end with EcoRI and 3' end with XhoI site"

BASE COUNT 137 a 95 c 148 g 193 t

ORIGIN
Alignment Scores:
Pred. No.: 5, 31e-55 Length: 573
Score: 490.00 Matches: 91
Percent Similarity: 89.668 Conservative: 13
Best Local Similarity: 78.458 Mismatches: 12
Query Match: 80.728 Indels: 0
Gaps: 0

US-09-786-715-4 (1-118) x A1778940 (1-573)

QY 3 SerSerGluGluGluValIleGlyCysHisSerValAspGluTrpLysGluInphe 22
Db 30 TCATCTGAGGAAGACAGTGAATCGGCTCCACAAAGCTTGAGAGAGTGAAGGTGCAGCTC 89

QY 23 GlnLysGlyValAspSerLysLeuValIleAspPheThrAlaSerTrpCysGly 42
|||||
Db 90 CAGAAAGGTGGAGACCAAAAACCTGGGGGTGGATTTACTGCTTCCGTGGCGGT 149
QY 43 ProCysArgPheIleAlaProIleLeuAlaIleValIleAspPheThrProHisValIle 62
|||||
Db 150 CCTGCGCGTTTATTTGCCCCCAATTCCTGTCACATTCGTAAGAAGATGCCCATGTATTAG 209
QY 63 PheLeuLysValAspValAspIleLeuLysThrValAlaIleGluPheLysValGluAla 82
Db 210 TTCCTCAAGGTTGATGTTGATGACACTGAGAAAGTTGCAGAGAAATGGAATGTGGAGCA 269
QY 83 MetProThrPheValPheLeuLysGluLysGluValGluAlaGluValGluAlaGly 102
Db 270 ATGCCAAGCTTTGTCTCTCAATTAAGAGGGTTAAAGAGTGAATGAGGTGTGTGTGCCAAT 329
QY 103 LysGluGluLeuGlnAlaThrValAlaGluLysHisGlyAlaIleThrAla 118
Db 330 AAGAGCGATTCCTTCAGACCATAGAGAGCATGTGCTGCTCTCTCTCT 377

RESULT 15
A1781827 573 bp mRNA linear EST 18-MAY-2001
LOCUS EST262706 tomato susceptible, Cornell Lycopersicon esculentum cDNA
DEFINITION clone CLES17C16, mRNA sequence.
ACCESSION A1781827
VERSION A1781827.1 GI:5279868
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 573)
REFERENCE D'Ascenzo,M., He,X., Lyman,J.J., Matero,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
C.L., Nieman,M., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Giovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas susceptible tomato
UNPUBLISHED
JOURNAL Contact: CUGI
COMMENT Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source
1..573
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="RI1-13 (Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="CLES17C16"
/tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
/clone_1lb="tomato susceptible, Cornell"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; CLES - Tomato Pseudomonas Susceptible EST library.
directionally cloned cDNAs inserted into pBluescript SK(-
) at 5' end with EcoRI and 3' end with XhoI site"

BASE COUNT 137 a 95 c 148 g 193 t

ORIGIN
Alignment Scores:
Pred. No.: 5, 31e-55 Length: 573
Score: 490.00 Matches: 91
Percent Similarity: 89.668 Conservative: 13
Best Local Similarity: 78.458 Mismatches: 12
Query Match: 80.728 Indels: 0
Gaps: 0

us-09-786-715-4 (1-118) x A1781827 (1-573)

```

QY      3 SerSerGluGluGlyGlnValIleGlyCysHisSerValAspGluTrpLysGluGlnPhe 22
      |||
Db      30 TCATCTGAGGAGGACAGAGTGCCTGCCACAGGTTGAGAGTGAAGTGCACGCTC 89
      |||
QY      23 GlnLysGlyValAspSerLysLysLeuValValIleAspPheThrAlaSerTrpCysGly 42
      |||
Db      90 CAGAGGGGTGAGAGACCAAAAGCTGGTGGTGGATTTACTGCTCCTGCTGCGGT 149
      |||
QY      43 ProCysArgPheIleAlaProIleLeuAlaGluMetAlaLysLysThrProHisValIle 62
      |||
Db      150 CCTTGCCGTTTATTGCCCCAATCTGCTGACATGCTAAGAGATGCCCATGTTATG 209
      |||
QY      63 PheLeuLysValAspValAspGluLeuLysThrValAlaGluGluPheLysValGluAla 82
      |||
Db      210 TTCCTCAAGGTTGATGTTGATGAACTGAGAAAGTTGCAGAGAAATGATGTGAGGCA 269
      |||
QY      83 MetProThrPheValPheLeuLysGluGlyLysGluValGluArgLeuValGlyAlaArg 102
      |||
Db      270 ATGCCAACTTTTCTTCATTAAAGAGGGTAAAGAGATGATAGGTTGTTGGTGCCTCAAT 329
      |||
QY      103 LysGluGluLeuGlnAlaThrValGluLysHisGlyAlaIleThrAla 118
      |||
Db      330 AAAGACGATTGCTTCAGACCATTAGAGAGCATGTGCTGCTGCT 377

```

Search completed: August 17, 2003, 23:34:15
 Job time : 1600.81 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 18:47:50 ; Search time 1856.4 Seconds

(without alignments)
2644.453 Million cell updates/sec

Title: US-09-786-715-6
Perfect score: 615
Sequence: 1 MAGSSEGOVISCHTVEEMN.....GAKKDELQOKIOKHVASASA 120

Scoring table: BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-O=/cgn2_1/USPTO/US09786715/runat_11082003_150514_6035/app_query.fasta_1.1052
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biolum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09786715.ecgn_1_1_5721_eunat_11082003_150514_6035 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -DSPELOCK=100 -LONGLOC
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pt:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_in:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rod:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	544	88.5	630	8	PSA310990
2	490	79.7	603	8	RCPTHIORXN
3	482	78.4	345	6	AX505468
4	482	78.4	480	8	AY088687
5	482	78.4	497	8	ATTHTIOARA
6	460	74.8	664	8	AE323593
7	456	74.1	698	8	NTPRNA
8	453	73.7	665	8	AY170650
9	445	72.4	653	6	AR016869
10	445	72.4	653	6	AR020895
11	445	72.4	653	6	AR027218
12	445	72.4	653	6	AR038505
13	445	72.4	653	6	AR064647
14	445	72.4	653	6	AR067572
15	445	72.4	653	6	I38524
16	445	72.4	653	6	I56999
17	445	72.4	653	6	I59865
18	445	72.4	653	6	I75192
19	434	70.6	784	8	AY271308
20	429	69.8	357	8	AY040028
21	429	69.8	528	8	ATTHRED4
22	429	69.8	530	8	AK118035
23	429	69.8	560	8	AY087159
24	429	69.8	561	8	AF360227
25	414	67.3	593	8	PSA319808
26	399	64.9	345	8	AF483265
27	388	63.1	526	11	G73679
28	388	63.1	601	8	OS092541
29	388	63.1	686	6	E08194
30	388	63.1	687	8	RICTH
31	385.5	62.7	590	8	AY088698
32	385	62.6	595	8	D87984
33	383	62.3	366	6	AX654096
34	381.5	62.0	360	6	AX505469
35	381.5	62.0	360	8	BT004710
36	381.5	62.0	556	8	AK118542
37	381	62.0	740	8	AB053294
38	378.5	61.5	642	8	ATTHRED1
39	376.5	61.2	357	6	AX412276
40	376.5	61.2	357	6	AX412277
41	376.5	61.2	357	6	AX412278
42	376.5	61.2	357	6	AX412279
43	376.5	61.2	357	6	AX412473
44	376.5	61.2	357	6	AX412474
45	376.5	61.2	357	6	AX412566

RESULT 1

ALIGNMENTS

PSA310990
LOCUS PSA310990 630 bp mRNA linear PLN 12-Apr-2001
DEFINITION Pisum sativum mRNA for thiorodoxin h (trhx gene).
ACCESSION AJ310990
VERSION AJ310990.1 GI:13624883
KEYWORDS thiorodoxin h; trhx gene.
SOURCE Pisum sativum (pea)
ORGANISM Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.

REFERENCE
AUTHORS Traverso, J.A.
JOURNAL Thesis (2001) Department of Bioquímica, Biología Celular y Molecular de Plantas, Estación Experimental del Zaidín (C.S.I.C.), Granada, Spain

REFERENCE
AUTHORS Traverso, J.A., Cazalis, R., Sahrawy, M., Lopez-Gorge, J. and Chueca, A.
JOURNAL Sequencing, cloning and expression of Pisum sativum thiorodoxin h
REFERENCE 3 (bases 1 to 630)
AUTHORS Traverso, J.A.
TITLE Direct Submission
JOURNAL Submitted (11-Apr-2001) Traverso J.A., Bioquímica Biología Celular y Molecular de plantas, Estación Experimental del Zaidín (CSIC), Profesor Alameda 1, Granada, 18008, SPAIN
location/Qualifiers

FEATURES
source 1..630
/organism="Pisum sativum"
/mol_type="mRNA"
/variety="Lincoln"
/db_xref="taxon:3888"
/tissue_type="leaves"
1..630
/gene="trhx"
36..398
/gene="trhx"
/function="Unknown"
/codon_start=1
/evidence="experimental"
/product="thiorodoxin h"
/protein_id="CAC36386.1"
/db_xref="GI:13624884"
/translation="MAGSSEGOVIVSCHSDVANDIIRHNEKSLIVDFATSMCGP
CRRIAPFLGELAKKPNVIFLKYVDDELKSVADMAVEAMPTFVFKEGII LKVVGA
KKRELQOTTERHVAASSNA"
398..609
/gene="trhx"
609
polyA_site /gene="trhx"
BASE COUNT 195 a 95 c 141 g 199 t
ORIGIN

Alignment Scores:
Pred. No.: 4..38e-55 Length: 630
Score: 544.00 Matches: 102
Percent Similarity: 95.00% Conservative: 12
Best Local Similarity: 85.00% Mismatches: 6
Query Match: 88.46% Indels: 0
Gaps: 0

US-09-786-715-6 (1-120) x PSA310990 (1-630)

OY 1 MetAlaGlySerSerGluGluGlnValIleSerCysHisThrValGluGluTyrPasn 20
DB 36 ATGGCAGGTTCAACAGAGGAGCAAGTTATCAGCTGCACAGCGCTTGATGATGAGAC 95
OY 21 AspGlnLeuGlnInuGlnGlnSerLysLysLeuIleValValAspPheThrAlaSer 40
DB 96 GATATCTTCACAGAGGAGCAATGATCCAGAAACTATTTGTTGGACTTTACTGCTTCT 155
OY 41 TTPCysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaIleLysPheThr 60

DB 156 TGGGTGACCAACGCGCTTCATTCGACCAATTCCTTGTAATGGCTAGAGATTACA 215
OY 61 SerValIlePheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTyrPala 80
DB 216 AATGTCATATTCCTTAAGGTGAGCGTGAGCAAGCAACTAAAGTCTGTGCTCAAGATTGGCT 275
OY 81 IleglualaMetProThrPheValPheValLysGluGluThrLeuLeuAspLysValVal 100
DB 276 GTTGAGGCTATGGCAACATTTGCTTTGTAAGAAGAGACGATTTTGGGCAAGTGCTT 335
OY 101 GlyAlaLysLysAspGluLeuGlnLysIleGlnLysHisValAlaSerAla 120
DB 336 GGAGCAAGAAAGAGAAAGCAAGTGCAGACATTTGAAGACATGTGCTTCATCTAATGCT 395

RESULT 2
RCHTHORXN 603 bp mRNA linear PLN 04-Apr-1996
LOCUS RCHTHORXN
DEFINITION R. communis mRNA for thiorodoxin.
ACCESSION Z70677
VERSION Z70677.1 GI:1255953
KEYWORDS thiorodoxin.
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.

REFERENCE
AUTHORS Szederkenyi, J., Dolgener, E. and Schnobelt, C.
JOURNAL cDNA expressed in Ricinus cotyledons
REFERENCE 2 (bases 1 to 603)
AUTHORS Dolgener, E.
TITLE Direct Submission
JOURNAL Submitted (04-Apr-1996) Dolgener E., University of Bayreuth, Department of Plant Physiology, Universitaetsstr.30, Bayreuth, Germany, 95440
location/Qualifiers

FEATURES
source 1..603
/organism="Ricinus communis"
/mol_type="mRNA"
/cultivar="Sanguineus"
/db_xref="taxon:3988"
/clone="PEDRH018"
/tissue_type="cotyledon"
/clone_lib="lambda Exclon"
/dev_stage="seedling"
23..379
/codon_start=1
/product="thiorodoxin"
/protein_id="CAA94534.1"
/db_xref="GI:1255954"
/db_xref="SRRREMBL:043636"
/translation="MAAEQGVIGCHTVEAMNEQLOKNDTKLIYVDFATSMCGP
FLAPFLAELAKKLPNTVFLKYVDDELKTVAHAEVAESMPTFME LKGGKIMDKVVGAK
DELQQTIAHKHMAAST"
379..603
/gene="trhx"
603
polyA_site /gene="trhx"
BASE COUNT 179 a 101 c 157 g 166 t
ORIGIN

Alignment Scores:
Pred. No.: 1..01e-48 Length: 603
Score: 490.00 Matches: 89
Percent Similarity: 91.38% Conservative: 17
Best Local Similarity: 76.72% Mismatches: 10
Query Match: 79.67% Indels: 0
Gaps: 0

US-09-786-715-6 (1-120) x RCHTHORXN (1-603)

OY 4 SerSerGluGluGlnValIleSerCysHisThrValGluGluTyrPasnAspGlnLeu 23
DB 26 GCAGCAGAGAGAGGAGGAGTGAATGGTGCACACATGTTGAGGACATGAATGAGCAATTG 85

QY 24 GlnLysGlyAsnGluSerLysLysLeuIleValAlaSpPheThrAlaSerTrpCysGly 43
 |||||.....||| |||||.....||| |||||.....||| |||||.....|||
 Db 86 CAGAAAGGAATGATACCAAGGACGATCGTTGTTGATTACTTCACTTCATGGTGGTA 145
 QY 44 ProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIle 63
 |||||.....||| |||||.....||| |||||.....||| |||||.....|||
 Db 146 CCATGCGCGTTTCATGCTCCCTTCTTGCTGAGCTGGCCAGAAATGCCAATGTTTACC 205.
 QY 64 PheLeuLysValAlaSpLysLysLeuLysSerValSerGlnAspTrpAlaIleGluAla 83
 |||||.....||| |||||.....||| |||||.....||| |||||.....|||
 Db 206 TTCCTGAAAGTGTGATGTGATGACGAGACTGTTGCTCAGACAGGCGCTGGAGTCA 265
 QY 84 MetProthPheValPheValLysGluGlyThrLeuLeuAspLysValAlaGlyAlaLys 103
 |||||.....||| |||||.....||| |||||.....||| |||||.....|||
 Db 266 ATGCCACCTTATATGTTCTCTGAAGGAGGGAAGATTATGACACAGGTGGTTGAGCAAG 325
 QY 104 LysAspGluLeuGlnGlnLysLysIleGlnLysHisValAlaSerAlaSer 119
 |||||.....||| |||||.....||| |||||.....||| |||||.....|||
 Db 326 AAAGACGACTGACGAACTATAGCGAAACACATGCTACTGCTCC 373
 RESULT 3
 AX505468
 LOCUS AX505468 345 bp DNA linear PAT 27-SEP-2002
 DEFINITION Sequence 163 from Patent WO0216655.
 ACCESSION AX505468
 VERSION AX505468.1 GI:23386705
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1
 Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
 Stress-regulated genes of plants, transgenic plants containing
 same, and methods of use
 Patent: WO 0216655-A 163 28-FEB-2002;
 JOURNAL The Scripps Research Institute (US) ; Syngenta Participations AG
 (CH)
 FEATURES
 source location/Qualifiers
 1..345
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 BASE COUNT 90 a 68 c 90 g 97 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4.65e-48 Length: 345
 Score: 482.00 Matches: 88
 Percent Similarity: 89.38% Conservative: 13
 Best Local Similarity: 77.88% Mismatches: 12
 Query Match: 78.37% Indels: 0
 Gaps: 0
 US-09-786-715-6 (1-120) x AX505468 (1-345)
 QY 4 SerSerGluGluGlyGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeu 23
 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 4 GCTTCGGAAGAGGACAACTGATCGCTCCACACCGCTGAGACATGGAACGACGACTT 63
 QY 24 GlnLysGlyAsnGluSerLysLysLeuIleValAlaSpPheThrAlaSerTrpCysGly 43
 |||||.....||| |||||.....||| |||||.....||| |||||.....|||
 Db 64 CAGAAAGGAATGATACCAAACTCTTGTGGTGGTTGATTCACGCGCTTGTGGTGGTA 123
 QY 44 ProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIle 63
 |||||.....||| |||||.....||| |||||.....||| |||||.....|||
 Db 124 CCATGCGCGTTTCATGCTCCCTTCTTGCTGATTCGCTAAGAACTCTCCTAAGCGCTT 183
 QY 64 PheLeuLysValAlaSpLysLysLeuLysSerValSerGlnAspTrpAlaIleGluAla 83
 |||||.....||| |||||.....||| |||||.....||| |||||.....|||
 Db 184 TTCCTGAAAGTGTGATGTGATGAAATTTGAAGTGGTGGCAAGATGCGCATACAGCGC 243

QY 84 MetProthPheValPheValLysGluGlyThrLeuLeuAspLysValAlaGlyAlaLys 103
 |||||.....||| |||||.....||| |||||.....||| |||||.....|||
 Db 244 ATGCCACCTTATATGTTCTCTGAAGGAGGGAAGATTATGACACAGGTGGTTGAGCAAG 303
 QY 104 LysAspGluLeuGlnGlnLysLysIleGlnLysHisValAla 116
 |||||.....||| |||||.....||| |||||.....||| |||||.....|||
 Db 304 AAAGATGAGCTTCAGCTCACTGACATTCGCCAACAACCTTGGCT 342
 RESULT 4
 AY088687
 LOCUS AY088687 480 bp mRNA linear PLN 14-APR-2003
 DEFINITION Arabidopsis thaliana clone 9189 mRNA, complete sequence.
 ACCESSION AY088687
 VERSION AY088687.1 GI:21407461
 KEYWORDS FLI_CDNA.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1 (bases 1 to 480)
 Haas, B.-J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N.,
 Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
 Full-length messenger RNA sequences greatly improve genome
 annotation
 JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)
 MEDLINE 22088475
 PUBMED 12093376
 REFERENCE 2 (bases 1 to 480)
 Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
 Feldmann, K.
 Full-length cDNA from Arabidopsis thaliana
 3 (bases 1 to 480)
 TITLES Unpublished
 JOURNAL 3 (bases 1 to 480)
 REFERENCE Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
 Feldmann, K.
 TITLES Direct Submission
 JOURNAL Submitted (11-MAR-2002) Ceres, Inc. 3007 Malibu Canyon Road,
 Malibu, CA 90265, USA
 COMMENT
 This clone sequence is one of 5,000 Ceres full-length cDNAs made
 available to TIGR and Genbank. The following quality assessment of
 this set was done by comparison with known proteins: two percent of
 the clones are estimated to be 5'-truncated; less than one percent
 are 3'-truncated; approximately two percent represent alternative
 splice variants, including unspliced introns and spliced exons; one
 percent may contain premature stop codons; five percent may have
 frame shifts in a coding region. A sequence is considered to be
 5'-truncated if it lacks the translation initiation start (ATG). A
 sequence is considered to be 3'-truncated if it lacks the
 C-terminal end of the encoded protein. Please note that these cDNA
 sequences are derived from the WS or Laer ecotypes and therefore
 may contain polymorphisms when compared to sequences from Col-0.
 Geneset carried out the library production and sequencing of the
 full-length clones. Ceres, Inc. carried out the clustering of the
 5' sequences, selection of clones, and sequence assembly.
 FEATURES
 source location/Qualifiers
 1..480
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="9189"
 13..357
 /codon_start=1
 /product="thioredoxin h"
 /protein_id="AA067008.1"
 /db_xref="GI:21617958"
 /translation="MASEEGQYIACHTVETMNEQLOKANEKTLVVDTTASMCPCR
 FLAPFADLAKKLPVLFKVDTELSKVASDWAQADPTTFKLEKGLIDRVVGAKK
 DELQSTIRAKHA"
 BASE COUNT 124 a 93 c 111 g 152 t
 ORIGIN
 Alignment Scores:

Pred. No.: 6,83e-48 Length: 480
 Score: 482.00 Matches: 88
 Percent Similarity: 89.38% Conservative: 13
 Best Local Similarity: 77.88% Mismatches: 12
 Query Match: 78.37% Indels: 0
 DB: 8 Gaps: 0

US-09-786-715-6 (1-120) x AY088687 (1-480)

QY 4 SerSerGluGluGlnGlnValIleSerCyshIsthrValGluGluGluTTPAsnAspGlnLeu 23
 Db 16 GCTTCGGAAGAGACAGATGATGCGCTGCCACACCGTTGAGACATGAGACGACGCTT 75
 QY 24 GlnLysGlnAsnGluSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGly 43
 Db 76 CAGAAAGCTATGATGATCAAAACCTGTGTGTGTTGTTTACAGCGCTCTGTGTGTGGA 135
 QY 44 ProcysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIle 63
 Db 136 CCATGTCGTTTCATCGCTCCATCTTCTTGATTTGGCTAAGAAACTTCCTAACGTCCTT 195
 QY 64 PheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAla 83
 Db 196 TTCCTCAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 255
 QY 84 MetProThrPheValAlaPheValLysGluGlyThrLeuLeuAspLysValAlaGlyAlaLys 103
 Db 256 ATGCCAACCTTCATGCTTTTGAAGAGAGGAGAGATTTTGACCAAGTTGTTGGAGCCAG 315
 QY 104 LysAspGluLeuGlnGlnLysIleGlnLysHisValAla 116
 Db 316 AAGATGAGCTTCAGTCTACCATTCGCCAACACATTGGCT 354

RESULT 5
 ATTHIOARA
 LOCUS 497 bp mRNA linear PLN 16-JUN-1994
 DEFINITION A.thaliana mRNA for thioredoxin H.
 ACCESSION 214084.1
 VERSION 214084.1 GI:16551
 KEYWORDS thioredoxin H.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 497)
 Nucleotide sequence of a cDNA clone encoding an Arabidopsis thaliana thioredoxin H
 Plant Physiol. 102 (1), 327-328 (1993)
 JOURNAL MEDLINE 94151431
 PUBMED 8108503
 REFERENCE 2 (bases 1 to 497)
 AUTHORS Meyer, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-1992) Yves Meyer PhD, Laboratoire de Physiologie vegetale, Universite de Perpignan, Av de Villeneuve 52, Perpignan, 66360, FRANCE
 FEATURES
 source location/Qualifiers
 1..497
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 30..374
 /codon_start=1
 /product="thioredoxin H"
 /protein_id="CAAT8462.1"
 /db_xref="GI:16552"
 /db_xref="SWISS-PROT:P29448"
 /translation="MASEEGVATCHVTETVEMNOLOKANESKTLVVVDFTASMGPCR FIAFPADLAKRLPNVLFKVDDELKSVASDMAIQAMTFPMFLKBECKILDKVYGAKK DELOSTIAKHLA"
 CDS
 BASE COUNT 135 a 94 c 116 g 152 t

ORIGIN
 Alignment Scores:
 Pred. No.: 7.11e-48 Length: 497
 Score: 482.00 Matches: 88
 Percent Similarity: 89.38% Conservative: 13
 Best Local Similarity: 77.88% Mismatches: 12
 Query Match: 78.37% Indels: 0
 DB: 8 Gaps: 0

US-09-786-715-6 (1-120) x ATTHIOARA (1-497)

QY 4 SerSerGluGluGlnGlnValIleSerCyshIsthrValGluGluGluTTPAsnAspGlnLeu 23
 Db 33 GCTTCGGAAGAGACAGATGATGCGCTGCCACACCGTTGAGACATGAGACGACGCTT 92
 QY 24 GlnLysGlnAsnGluSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGly 43
 Db 93 CAGAAAGCTATGATGATCAAAACCTGTGTGTGTTGTTTACAGCGCTCTGTGTGTGGA 152
 QY 44 ProcysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIle 63
 Db 153 CCATGTCGTTTCATCGCTCCATCTTCTTGATTTGGCTAAGAACTTCTTAACGTCCTT 212
 QY 64 PheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAla 83
 Db 213 TTCCTCAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 272
 QY 84 MetProThrPheValAlaPheValLysGluGlyThrLeuLeuAspLysValAlaGlyAlaLys 103
 Db 273 ATGCCAACCTTCATGCTTTTGAAGAGAGGAGAGATTTTGACCAAGTTGTTGGAGCCAG 332
 QY 104 LysAspGluLeuGlnGlnLysIleGlnLysHisValAla 116
 Db 333 AAGATGAGCTTCAGTCTACCATTCGCCAACACATTGGCT 371

RESULT 6
 AF323593
 LOCUS 664 bp mRNA linear PLN 02-NOV-2001
 DEFINITION Prunus persica thioredoxin H mRNA, complete cds.
 ACCESSION AF323593
 VERSION AF323593.1 GI:16588842
 KEYWORDS Prunus persica (peach)
 SOURCE Prunus persica
 ORGANISM Prunus persica
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 1 (bases 1 to 664)
 Callahan, A.M., Morgens, P.H. and Cohen, R.A.
 Isolation and initial characterization of cDNAs for mRNAs regulated during peach fruit development
 J. Am. Soc. Hortic. Sci. 118, 531-537 (1993)
 REFERENCE 2 (bases 1 to 664)
 AUTHORS Callahan, A.M., Morgens, P.H., Cohen, R.A. and Scorza, R.
 TITLE Regulation of peach gene expression in a peach/almond hybrid
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 664)
 AUTHORS Callahan, A.M., Dunn, L.L. and Cohen, R.A.
 TITLE Direct Submission
 JOURNAL Submitted (22-NOV-2000) USDA-ARS, Appalachian Fruit Research Station, 45 Wiltshire Rd., Kearneysville, WV 25430, USA
 FEATURES
 source location/Qualifiers
 1..664
 /organism="Prunus persica"
 /mol_type="mRNA"
 /cultiivar="B612615"
 /db_xref="taxon:3760"
 /clone="poch306c"
 /tissue_type="ripe fruit"
 71..481
 /codon_start=1
 /product="thioredoxin H"

/protein_id="AL26915.1"
 /db_xref="GI:1658843"
 /translation="MAEPNOVIGCHTTOAEQOLHKENKKLVVDPAASMGPCRL
 IAPIILAEKKTPEYVFLKYVDDELTVSEKGVEMPTFLFKKGIYDKVGAKKD
 ELQIKYAKHVAHAASATASATASATATATATATA"

BASE COUNT 182 a 147 c 161 g 174 t

ORIGIN

Alignment Scores:

Pred. No.: 3,98e-45 Length: 664
 Score: 460.00 Matches: 83
 Percent Similarity: 86.21% Conservative: 17
 Best Local Similarity: 71.55% Mismatches: 16
 Query Match: 74.80% Indels: 0
 DB: Gaps: 0

US-09-786-715-6 (1-120) x AF323593 (1-664)

QY 5 SerGluGluGlyGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeuGln 24
 :||||| :||||| :||||| :||| :|||||
 Db 74 GCGAGGAAATCAATCAATCGGCTGCCACACACAGCCCTGGAAGAGCAGCTCCAT 133
 QY 25 LysGlyAsnGluSerLysLysLeuValAspPheThrAlaSerTrpCysGlyPro 44
 :||||| :||||| :||||| :||||| :|||||
 Db 134 AAGGAAACGAGAAACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 193
 QY 45 CysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIlePhe 64
 :||||| :||||| :||||| :||||| :|||||
 Db 194 TGGCGGTGATCCGCCCAATCTTGCGGAGTGTGGCTGAAGAGCCCAAGAGAGCTTC 253
 QY 65 LeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAlaMet 84
 :||||| :||||| :||||| :||||| :|||||
 Db 254 CTAAGAGTGGACGTGATGATGAGACGTTCCTCCAGAGAGTGGGGTGTGAGAGCAG 313
 QY 85 ProThrPheValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLysLys 104
 :||||| :||||| :||||| :||||| :|||||
 Db 314 CCTACCTCTCTCTCTCTCAAGAGAGAGATGTGACACAGCTGTGGTGGCCAGAGAA 373
 QY 105 AspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSerAla 120
 :||||| :||||| :||||| :||||| :|||||
 Db 374 GACGATTTACATCATCAAGTTGCCAAGCATGTGCGCGCGCGCT 421

RESULT 7
 NTRNA 698 bp mRNA linear PLN 15-FEB-1994

LOCUS N. tabacum mRNA for thioredoxin.
 ACCESSION X58527.1 GI:20046

VERSION X58527.1 GI:20046
 KEYWORDS thioredoxin.
 SOURCE Nicotiana tabacum (common tobacco)
 ORGANISM Nicotiana tabacum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.

REFERENCE
 AUTHORS Marty,I. and Meyer,Y.
 TITLE Nucleotide sequence of a cDNA encoding a tobacco thioredoxin
 JOURNAL Plant Mol. Biol. 17 (1), 143-147 (1991)

MEDLINE
 PUBMED 91328721
 1868216

REFERENCE
 AUTHORS 2 (bases 1 to 698)
 TITLE Bruidou,C., Marty,I., Chatlier,Y. and Meyer,Y.
 The Nicotiana tabacum genome encodes two cytoplasmic thioredoxin

genes which are differentially expressed

JOURNAL Mol. Gen. Genet. 238 (1-2), 285-293 (1993)

MEDLINE
 PUBMED 93241165
 8479434

REFERENCE
 AUTHORS 3 (bases 1 to 698)
 TITLE Meyer,Y.
 Direct Submission

JOURNAL Submitted (14-FEB-1991) Y. Meyer, Laboratoire de Physiologie et
 Biology, Moleculaire Vegetale, Universite av de Villeneuve, 66860
 Perpignan, France

COMMENT Gene product is probably cytoplasmic.
 FEATURES Location/Qualifiers
 source 1..698

/organism="Nicotiana tabacum"
 /mol_type="mRNA"
 /strain="white Burley"
 /db_xref="taxon:4097"
 /clone_lib="plasmid pT219"
 /dev_stage="in vitro cells"
 1..682
 /evidence=experimental
 79..459
 /codon_start=1
 /product="thioredoxin"
 /protein_id="CAA41415.1"
 /db_xref="GI:20047"
 /db_xref="SWISS-PROT:P29449"
 /translation="MAANDATSEEGQVFGCHKEEMNEFKGVETKRLVVDPFAS
 WCGPREFIPIADIARKMPHVFLKYVDDELTVSAEMSVEMPTFVLKDGKEVDK
 VVGAKKEELQGITVKAAPATVTA"

CDs
 mRNA
 CDS

polysignal
 polysignal
 polysignal
 BASE COUNT 192 a 117 c 164 g 225 t

ORIGIN

Alignment Scores:

Pred. No.: 1.25e-44 Length: 698
 Score: 456.00 Matches: 84
 Percent Similarity: 84.75% Conservative: 16
 Best Local Similarity: 71.19% Mismatches: 18
 Query Match: 74.15% Indels: 0
 DB: Gaps: 0

US-09-786-715-6 (1-120) x NTRNA (1-698)

QY 2 AlaGlySerSerGluGluGlnValIleSerCysHisThrValGluGluTrpAsnAsp 21
 :||| :||||| :||||| :||||| :|||||
 Db 94 GCTACTTTCATCCAGAGAGGACAAAGTTCGCTGCCACAGAGTTGAGGATGAGAGCAG 153
 QY 22 GlnLeuGlnLysGlnLysSerLysLysLeuValValAspPheThrAlaSerTrp 41
 :||||| :||||| :||||| :||||| :|||||
 Db 154 TACTTCAGAAAGAGCGGTGAGACTAAGAACTGCTGCTGCTGCTGCTGCTGCTGCTG 213
 QY 42 CysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSer 61
 :||||| :||||| :||||| :||||| :|||||
 Db 214 TGGGCGCTTGGCGGTTTATTTGCCCCCAATTCCTTGACATTTGCTAAGAGAGTCCCAT 273
 QY 62 ValIlePheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIle 81
 :||||| :||||| :||||| :||||| :|||||
 Db 274 GTTATATTCCTCAAGGTGATGTGTTGATGAACCTGAAGAGTTCACCGGAGATGAGTGTG 333
 QY 82 GluAlaMetProThrPheValPheValLysGluGlyThrLeuLeuAspLysValValGly 101
 :||||| :||||| :||||| :||||| :|||||
 Db 334 GAGCAATGCACTTTTCTTCATTAAAGATGAAGAAAGATGACAGAGTGTGTGT 393
 QY 102 AlaLysLysAspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSer 119
 :||||| :||||| :||||| :||||| :|||||
 Db 394 GCCAAGAAAGAGAGTTCAGACACCATAGTAGAGCATGCTCTCTCTACT 447

RESULT 8
 LOCUS AY170650 665 bp mRNA linear PLN 02-JAN-2003

DEFINITION Pisum sativum clone 3 thioredoxin h mRNA, complete cds.
 ACCESSION AY170650
 VERSION AY170650.1 GI:27466893

KEYWORDS
 SOURCE Pisum sativum (pea)
 ORGANISM Pisum sativum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
 Pisum.

REFERENCE 1 (bases 1 to 665)
AUTHORS Montichard,F., Renard,M., Duval,F.D. and Machere,J.D.
TITLE Expression of the NADP-thioredoxin reductase/thioredoxins h system during germination of seeds of Pisum sativum L
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 665)
AUTHORS Montichard,F., Renard,M., Duval,F.D. and Machere,J.D.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-2002) UMR 1191 Physiologie Molculaire des Semences, UFR Sciences, 16 bd Lavoisier, Angers 49045, France

FEATURES
source
Location/Qualifiers
1..665
/organism="Pisum sativum"
/mol_type="mRNA"
/db_xref="taxon:3888"
/clone="3"
74..415
/note="trx h"
/codon_start=1
/product="thioredoxin h"
/protein_id="AA012854.1"
/db_xref="GI:27466894"
/translation="MABEGYIGVHTYDAKEQLEKSKKLLVDFPTSMGCPKRE IAPILAIKALHIVFLKVDVDELKTVSEWGLEAMPTFLKDGELVDKVGAKKE ELQKIDKHAA"

BASE COUNT 220 a 85 c 164 g 196 t
ORIGIN

Alignment Scores:
Pred. No.: 2.68e-44 Length: 665
Score: 453.00 Matches: 84
Percent Similarity: 86.61% Conservative: 13
Best Local Similarity: 75.00% Mismatches: 15
Query Match: 73.66% Indels: 0
DB: 8 Gaps: 0

US-09-786-715-6 (1-120) x AY170650 (1-665)

QY 5 SerGluGluGlyGlnValIleSerCysHisThrValGluGluTrpAsnAspGlnLeuGln 24
Db 77 GCGGAGAGGAGGACAGATGCGTGTCCACACCGTGTGAGAGGACATGTACAG 136
QY 25 LysGlyAsnGluSerLysLysLeuIleValAlaAspPheThrAlaSerTrpCysGlyPro 44
Db 137 AAGGGAAGCCCTCAAGAAACTGATGTATTCACCTCTTGTGCGGTCGA 196
QY 45 CysArpPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIlePhe 64
Db 197 TGCCGTTTATTTGCCCAATTTTGGCAGAGATTGCTTAAAGCTTACACATGTACCTTTC 256
QY 65 LeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAlaMet 84
Db 257 CTTAAGGTTGACGCGATGATGAATGAGACTGTTCCGAGAGCGGCAATTGAAGCTATG 316
QY 85 ProThrPheValAlaPheValLysGluGlyThrLeuLeuAspLysValAlaGlyAlaLysLys 104
Db 317 CCAACATCTTCTGCTTGAAGAGATGTCGACCTTGCAACAAGCTTGGGTCACAGAAG 376
QY 105 AspGluLeuGlnGlnLysIleGlnLysHisValAla 116
Db 377 GAGGAGCTGCATTTGAATAATTGACACAGCATGCACT 412

RESULT 9
LOCUS ARO16869 653 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 103 from patent US 5777200.
ACCESSION ARO16869
VERSION ARO16869.1 GI:3973146
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 653)

AUTHORS Ryals,J.A., Alexander,D.C., Goodman,R.M. and Stinson,J.R.
TITLE Chemically regulatable and anti-pathogenic DNA sequences and uses
JOURNAL Patent: US 5777200-A 103 07-JUL-1998:
FEATURES
source
Location/Qualifiers
1..653
/organism="unknown"

BASE COUNT 165 a 114 c 157 g 215 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 2.32e-43 Length: 653
Score: 445.00 Matches: 84
Percent Similarity: 84.87% Conservative: 17
Best Local Similarity: 70.59% Mismatches: 17
Query Match: 72.36% Indels: 1
DB: 6 Gaps: 0

US-09-786-715-6 (1-120) x ARO16869 (1-653)

QY 2 AlaGlySerSerGluGluGlnValIleSerCysHisThrValGluGluTrpAsnAsp 21
Db 63 GCTACTTCATCCGAGAGGAGGACAGATGTCGCTGCCACAGGTTGAGCAATGAGACAG 122
QY 22 GlnLeuGlnLysGlyAsnGluSerLysLysLeuIleValAlaAspPheThrAlaSerTrp 41
Db 123 TACTCAAGAAAGCGTTCACATCAAGAACTGGTGGTGCATTTACTGCTTCATGCG 182
QY 42 CysGlyProCysArpPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSer 61
Db 183 TGCAGGSCCTTCCCTTTATTTGCCCCCAATTCCTGTCGATGCTTAAAGATGCCCCAT 242
QY 62 ValIlePheLeuLysValAspValAspGluLeuLysSerValSer-GlnAspTrpAlaIle 81
Db 243 GTTATATTCCTCAAGCTTGTGATGATGACACTGCAAGACTGTTTACGCGAATGAGACT 302
QY 81 eGluAlaMetProThrPheValAlaPheValLysGluGlyThrLeuLeuAspLysValAla 101
Db 303 GAGAGCAATGCCACATTTTCTTCATTAAGATGGAAGAAAGTGCAGACATGTTGTTGG 362
QY 101 ValLysLysAspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSer 119
Db 363 TGCCAGAAAGAGGAGTTCAGACACCAATGATGAGACATGCTCTCTGCTACT 417

RESULT 10
LOCUS ARO20895 653 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 103 from patent US 5789214.
ACCESSION ARO20895
VERSION ARO20895.1 GI:3975510
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 653)
AUTHORS Ryals,J.A., Friedrich,L.B., Uknes,S.J. and Ward,E.R.
TITLE Method of inducing gene transcription in a plant
JOURNAL Patent: US 5789214-A 103 04-AUG-1998:
FEATURES
source
Location/Qualifiers
1..653
/organism="unknown"

BASE COUNT 165 a 114 c 157 g 215 t 2 others
ORIGIN

Alignment Scores:
Pred. No.: 2.32e-43 Length: 653
Score: 445.00 Matches: 84
Percent Similarity: 84.87% Conservative: 17
Best Local Similarity: 70.59% Mismatches: 17
Query Match: 72.36% Indels: 1
DB: 6 Gaps: 0

US-09-786-715-6 (1-120) x ARO20895 (1-653)

OY		2	AlaGlySerSerGIUGlUGlValIleSerCysHISrRValIGlUGlUTPrAsnSP	21
Dd		63	GCTACTTCATCCGAGGAGGGACAAAGTGTCCGCTGCCAACAGTTGAGGAATGAGACGAG	122
OY		22	GlIneUGlnLysGLyASnglUserLysLysLeuileValValAASPheThAlaSerTrp	41
Dd		123	TACTTCAAAGAAAGCGGTGAGACTAAGAACACTGGTGGTGCGATTTCAGCTTCATCG	182
OY		42	CysGLyProCYSAIgpPheIIleAlaAPropheuAlaGlUleuAlALySLysPherThSer	61
Dd		183	TGCAGSCTTCGCCGTTTTATTATGGCCCCCAATTTCTCTGCATTCGTAAAGAAATGCCCAT	242
OY		62	VallIephelEuLyVaLaSPvaLaSPglUleuLYSSerValSer - GlNaSPTrPaLaI	81
Dd		243	GTTATATTCCCAAGGTGATTGATGATCACTGAAGACTGTTTACAGCGGAATGGAGTGT	302
OY		81	eGUaLaMeRProThrPheValIlePheValLysGLUGlYThrLeuEuaSpLyVaLaGl	101
Dd		303	GGAGGCAATGCCCACTTTGTCTTCATAAAGATGAAAAGAAAGATGGACAGAGTGTGG	362
OY		101	yAlALySLysApGlUenGlnGLyLIleGlnLHisHISValAlaSerAlaSer	119
Dd		363	TGCCAAGAAAGAGAGTTCACAGCACACCACATGTAAGAGCATCTGCTCTGCTACT	417
RESULT 11				
AR027218			653 bp	DNA linear PAT 29-SEP-1999
LOCUS				
DEFINITION			Sequence 103 from patent US 5856154.	
ACCESSION			AR027218	
VERSION			AR027218.1	GI:5938058
KEYWORDS				
SOURCE			Unknown.	
ORGANISM			Unclassified.	
REFERENCE			1 (bases 1 to 653)	
ADTHORS			Ryals,J.A., Alexander,D.C., Goodman,R.M. and Ward,E.R.	
TITLE			Method of protecting plants from comycete pathogens	
JOURNL			Patent: US 5856154-A 103 05-JUN-1999;	
FEATURES			location/qualifiers	
source			1..653	
BASE COUNT			165 a 114 c 157 g 215 t 2 others	
ORIGIN			/organism="unknown"	
Alignment Scores:				
Pred. No.:			2.32e-43	Length: 653
Score:			445.00	Matches: 84
Percent Similarity:			84.87%	Conservative: 17
Best local Similarity:			70.59%	Mismatches: 17
Query Match:			72.36%	Indels: 1
DB:			6 gaps:	0
US-09-786-715-6 (1-120) x AR027218 (1-653)				
OY		2	AlaGlySerSerGIUGlUGlValIleSerCysHISrRValIGlUGlUTPrAsnSP	21
Dd		63	GCTACTTCATCCGAGGAGGGACAAAGTGTCCGCTGCCAACAGTTGAGGAATGAGACGAG	122
OY		22	GlIneUGlnLysGLyASnglUserLysLysLeuileValValAASPheThAlaSerTrp	41
Dd		123	TACTTCAAAGAAAGCGGTGAGACTAAGAACACTGGTGGTGCGATTTCAGCTTCATCG	182
OY		42	CysGLyProCYSAIgpPheIIleAlaAPropheuAlaGlUleuAlALySLysPherThSer	61
Dd		183	TGCAGSCTTCGCCGTTTTATTATGGCCCCCAATTTCTCTGCATTCGTAAAGAAATGCCCAT	242
OY		62	VallIephelEuLyVaLaSPvaLaSPglUleuLYSSerValSer - GlNaSPTrPaLaI	81
Dd		243	GTTATATTCCCAAGGTGATTGATGATCACTGAAGACTGTTTACAGCGGAATGGAGTGT	302
OY		81	eGUaLaMeRProThrPheValIlePheValLysGLUGlYThrLeuEuaSpLyVaLaGl	101
Dd		303	GGAGGCAATGCCCACTTTGTCTTCATAAAGATGAAAAGAAAGATGGACAGAGTGTGG	362
OY		101	yAlALySLysApGlUenGlnGLyLIleGlnLHisHISValAlaSerAlaSer	119
Dd		363	TGCCAAGAAAGAGAGTTCACAGCACACCACATGTAAGAGCATCTGCTCTGCTACT	417

Db	303	GGAGGCAATGCCA	ACTTTTGTCTTCATTAAGAATGGAAGAAAGAGTGACAGACAGTTGTCG	362
Qy	101	YALALysLysAsp	GLuLeuGlnLysILeGlnLysHisValAlaSerAlaSer	119
Db	363	TGCCAAGAAAGAG	GTTCGACAGACCATAGTGAAGCATCTGCTCCTGCTACT	417
RESULT 12				
LOCUS	AR038505		653 bp	DNA
DEFINITION	Sequence 103 from patent US 5804693.		linear	PAT 29-SEP-1999
ACCESSION	AR038505			
VERSION	AR038505.1	GI:5957222		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 653)			
AUTHORS	Gaffney,T.D., Ryals,J.A., Friedrich,L.B., Uknes,S.J., Ward,E.R., Kessmann,H. and Verrooij,B.T.			
TITLE	Chemically regulatable and anti-pathogenic DNA sequences and uses thereof			
JOURNAL	Patent: US 5804693-A 103 08-SEP-1998;			
FEATURES	Location/Qualifiers			
source	1..653			
BASE COUNT	165 a 114 c 157 g 215 t		2 others	
ORIGIN	/organism="unknown"			
Alignment Scores:				
Pred. No.:	2.32e-43	Length:	653	
Score:	445.00	Matches:	84	
Percent Similarity:	84.87%	Conservative:	17	
Best Local Similarity:	70.59%	Mismatches:	1	
Query Match:	72.36%	Indels:	1	
DB:	6	Gaps:	0	
US-09-786-715-6 (1-120) x AR038505 (1-653)				
Qy	2	AlaGlySerSerGluGluGlnValILeSerCysHisThrValGluGluTrpAsn	21	
Db	63	GCTACTTCATCCGAGGAGGACAGAGTGTGGCTGCCACAGGTTGAGGATGACGAG	122	
Qy	22	GlnLeuGlnLysGlnGluSerLysLysLeuIleValValAspPheThrAlaSer	41	
Db	123	TACTTCAAGAAAGCGTTGAGACACPAAGAACTGGTGGTCGATTTTACTGCTTCATCG	182	
Qy	42	CysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysPheThrSer	61	
Db	183	TGGGSGCCTTCCCGTTATTATGCCCACTTCTCTGACATTTGCTAAGAAATGCCCCAT	242	
Qy	62	ValIlePheLeuLysValAspValAspGluLeuLysSerValSer-GlnAspTrpAla	81	
Db	243	GTTTATATTCCTCAAGGTTGATGTTGATGAACCTGTAAGACACTGTTTCAGCGGCAATGAGTGT	302	
Qy	81	eGluAlaMetProThrPheValPheValLysGluGlyThrLeuLeuAspLysValIle	101	
Db	303	GGAGGCAATGCCA	ACTTTTGTCTTCATTAAGAATGGAAGAAAGAGTGACAGACAGTTGTCG	362
Qy	101	YALALysLysAspGluLeuGlnLysILeGlnLysHisValAlaSerAlaSer	119	
Db	363	TGCCAAGAAAGAG	GTTCGACAGACCATAGTGAAGCATCTGCTCCTGCTACT	417
RESULT 13				
LOCUS	AR064647		653 bp	DNA
DEFINITION	Sequence 103 from patent US 5847258.		linear	PAT 29-SEP-1999
ACCESSION	AR064647			
VERSION	AR064647.1	GI:5993955		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 653)			


```

Qy      81  eglualametProthrPheValPheValIysGluGlyThrLeuLeuAspLysValValGI 101
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      303  GAGGCAATGCCAATCTTTGCTCTCTCATTTAAAGATGAGAAAGAGAGTGCACAGAGTTGTTGG 362

Qy      101  yAlaIysLysAspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSer 119
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      363  TGCACAGAAAGAGAGAGTTGCACAGACATAGTGAAGCATGCTGCTGCTACT 417

```

Search completed: August 17, 2003, 21:41:56
 Job time : 1858.4 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 17, 2003, 17:46:53 ; Search time 168.696 seconds
(without alignments)
1920.219 Million cell updates/sec

Title: US-09-786-715-6
Perfect score: 615
Sequence: 1 MAGSSEGGVTSCHTVEEMN.....GAKKDELOQIKKHVASASA 120

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame_plus_p2n.model -DEV=tlp
-Q=/gen2.1/USPTO_spool/US09786713/runat.11082003.150513.6025/app_query.fasta.1.1052
-DB=N.Geneseq.19Jun03 -QFMT=fastep -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdl
-LIST=45 -DOCALLING=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09786713.ecgn.1.1.874@runat.11082003.150513.6025 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: N.Geneseq.19Jun03:*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
26: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	615	100.0	738	21	AAZ51739	Glycine max thior
2	485	78.9	3888	24	ABSS3097	DNA encoding Thior
3	485	78.9	3888	24	ABN89581	Phaseolin promoter
4	482	78.4	345	24	ABZ12358	Arabidopsis thalia
5	482	78.4	345	24	ABN89587	Arabidopsis thalia
6	482	78.4	561	21	AAC51522	Arabidopsis thalia
7	482	78.4	563	21	AAC34121	Arabidopsis thalia
8	482	78.4	3129	24	ABSS3095	DNA encoding thior
9	482	78.4	3129	24	ABN89579	Phaseolin promoter
10	482	78.4	3888	24	ABSS3096	DNA encoding Oleos
11	482	78.4	3888	24	ABN89580	Phaseolin promoter
12	478	77.7	470	21	AAC37781	Arabidopsis thalia
13	477	77.6	4935	24	ABN89586	Promoter-Oleosin t
14	472	76.7	509	22	ABN87768	Peppermint plant o
15	445	72.4	653	16	AAO99783	Plant SAR gene pl.
16	445	72.4	653	20	AAV62799	Tobacco SAR CHX in
17	445	72.4	653	20	AAV81683	Tobacco protein-sy
18	438	71.2	402	25	ABX21664	Human GDP-mannose
19	430	69.9	574	21	AAZ51738	Catalpa speciosa t
20	429	69.8	560	21	AAC41961	Arabidopsis thalia
21	424	68.9	392	25	ABX18045	Human GDP-mannose
22	410	66.7	601	21	AAZ51740	Glycine max thior
23	408	66.3	328	21	AAA31097	Plant microsateili
24	403	65.5	346	21	AAA31096	Plant microsateili
25	398	64.7	320	21	AAA31785	Plant microsateili
26	382	63.7	614	21	AAZ51741	Vernonia mespilifo
27	381	63.6	390	25	ABX19403	Human GDP-mannose
28	388	63.1	686	15	AAO78205	Gene coding for pr
29	388	63.1	687	21	AAC66375	Rice thioridoxin h
30	385.5	62.7	590	21	AAC38792	Arabidopsis thalia
31	381.5	62.0	360	24	ABZ12359	Arabidopsis thalia
32	376.5	61.2	357	24	ABZ13931	Arabidopsis thalia
33	376.5	61.2	480	21	AAC36542	Arabidopsis thalia
34	376.5	61.2	524	21	AAC33829	Arabidopsis thalia
35	376.5	61.2	563	21	AAC34211	Arabidopsis thalia
36	376.5	61.2	652	21	AAC48656	Arabidopsis thalia
37	376.5	61.1	292	21	AAA31978	Plant microsateili
38	368	59.8	393	17	AAT10451	Hard wheat thiorid
39	368	59.8	393	21	AAC62457	Wheat thioridoxin
40	367	59.7	382	21	AAC62456	Soft wheat thiorid
41	367	59.7	384	17	AAT10450	Plant microsateili
42	367	59.7	419	21	AAA31942	Arabidopsis thalia
43	367	59.7	572	21	AAC52069	Arabidopsis thalia
44	366	59.5	870	21	AAZ51737	Momordica charanti
45	364.5	59.3	576	25	ABX56868	Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AAZ51739	
ID	AAZ51739 standard; cDNA: 738 BP.
AC	AAZ51739;
XX	XX
DT	04-JUL-2000 (first entry)
XX	XX
DE	Glycine max thioridoxin cDNA-1.
XX	XX
KW	Glycine max thioridoxin; clone sahic.pk001.117; chimeric gene; soybean;
XX	XX
OS	transgenic plant; seed storage protein; allergenicity; ss.
XX	XX
FT	Glycine max.
XX	XX
Key	Location/Qualifiers
CDS	68..430

```

FT      /*tag= a
FT      /product= "thioredoxin"
XX
XX      WO200014239-A2.
XX
XX      16-MAR-2000.
XX
XX      07-SEP-1999; 99WO-US20420.
XX
XX      08-SEP-1998; 98US-0099501.
XX
XX      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX      Allen SM, Thorpe CJ, Lu AL;
XX
XX      WPI: 2000-256987/22.
XX
XX      P-PSDB: AAY70481.
XX
XX      New isolated polynucleotide encoding thioredoxin polypeptide is useful
XX      for producing transgenic plants with an altered level of thioredoxin -
XX
XX      Claim 3; Page 30; 33pp: English.
XX
XX      The present CDNA sequence encodes glycine max thioredoxin protein. The
XX      cDNA was derived from clone sahic.pk001.117, which was isolated from a
XX      cDNA library prepared from soybean tissue sprayed with authority
XX      herbicide. Chimeric genes encoding all or a portion of the thioredoxin
XX      protein, in sense or antisense orientation are constructed, wherein
XX      expression of the chimeric gene results in production of altered levels
XX      of the thioredoxin protein in a transformed host cell. Thioredoxin is
XX      involved in the disassembly of seed storage proteins during germination
XX      by reducing S-S bonds and in the bread making process. Over expression of
XX      thioredoxin in cereals may reduce the allergenicity of any transgenic
XX      protein engineered into cereal crops with high sulphydryl content.
XX
XX      Sequence 738 BP; 260 A; 120 C; 146 G; 212 T; 0 other:
XX
XX      Alignment Scores:
XX      Pred. No.: 4,7e-73 Length: 738
XX      Score: 615.00 Matches: 120
XX      Percent Similarity: 100.00% Conservative: 0
XX      Best Local Similarity: 100.00% Mismatches: 0
XX      Query Match: 100.00% Indels: 0
XX      DB: 21 Gaps: 0
XX
XX      US-09-786-715-6 (1-120) x AAZ51739 (1-738)
XX
XX      1 MetAlaGlySerSerGluGluGlnValIleSerCysHisThrValGluGluTyrAsn 20
XX      68 ATGGCTGGCTATCGAAGAGGCAAGTCATTAGTCCACACCGTTGAAGATGGAAC 127
XX      21 AspGlnLeuGlnIlysgIyAsnGluSerIySlyLeuIleValValAspPheThrAlaSer 40
XX      128 GATCAACTCCAGAAAGGCAACGAATCCAAAGAACTCTTGTGTGGATTACTGCTTCT 187
XX      41 TrpCysGlyProCysArgPheIleAlaIleProPheLeuAlaGluLeuAlaIySlySphThr 60
XX      188 TGGTGTGGACCATGGCCCTTCATTGACACATTCTTGGCTGAGCGGCTAAGAAGTTACA 247
XX      61 SerValIlePheLeuIySlyValAspValAspGluLeuIySlySerValSerGlnAspTyrAla 80
XX      248 AGTGTCTATTTCCTAAAGGTGAGATGAGCAAGTAAGAGTGTCTCAAGATGGGCT 307
XX      81 IlleGluAlaMetProThrPheValAlaPheValIyGluIyThrLeuLeuAspIySlyVal 100
XX      308 ATTGAGGCTATGCCCACTTTTGTGTGTGTAAGAGGAAACGCTTCGGCAAAAGTGTG 367
XX      101.GIyAlaIySlyAspGluLeuGlnGlnIySlyIleGlnIyHisValAlaSerAlaSerAla 120
XX      368 GGAGCAAAAGAGATGAGTGTGACGACGAATAATACAGAAACATGAGCTTCAGCTAGTGT 427

```

```

ID      ABS53097 standard; DNA; 3888 BP.
XX
XX      ABS53097;
XX
XX      29-NOV-2002 (first entry)
XX
XX      DNA encoding Thioredoxin-oleosin fusion protein.
XX
XX      Thioredoxin; thioredoxin reductase; gene expression; oleosin;
XX      oil body; oleosin-thioredoxin fusion protein; gene; ds.
XX
XX      Arabidopsis thaliana.
XX
XX      Brassica napus.
XX
XX      Synthetic.
XX
XX      Key Location/Qualifiers
XX      CDS 1555..2658
XX
XX      /*tag= a
XX      /product= "Thioredoxin-oleosin fusion protein"
XX      exon 1555..2250
XX      /*tag= b
XX      /number= 1
XX      intron 2251..2489
XX      /*tag= c
XX      /number= 1
XX      exon 2490..2658
XX      /*tag= d
XX      /number= 2
XX
XX      US2002088025-A1.
XX
XX      04-JUL-2002.
XX
XX      03-JUL-2001; 2001US-0897425.
XX
XX      22-FEB-1991; 91US-0659835.
XX      16-NOV-1993; 93US-0142418.
XX      30-DEC-1994; 94US-0366783.
XX      25-APR-1997; 97US-0846021.
XX      18-DEC-1998; 98US-0210843.
XX
XX      (MOLO/) MOLONEY M M.
XX      (DALM/) DALMIA B K.
XX
XX      Moloney MM, Dalmia BK;
XX
XX      WPI: 2002-635723/68.
XX
XX      Expressing protein, by introducing chimeric nucleotide regulatory
XX      sequence, sequence encoding fusion protein, having sequence encoding
XX      protein, oleosin gene and sequence encoding termination region and
XX      producing protein -
XX
XX      Example 21; Fig 14; 69pp: English.
XX
XX      The invention describes a method of expressing thioredoxin or thioredoxin
XX      reductase (1) in the oil body of a host cell using an oil body protein
XX      gene. The method involves introducing a chimeric nucleic acid comprising
XX      a first sequence to regulate transcription, a second DNA sequence
XX      encoding a fusion polypeptide, comprising a sequence encoding an oleosin
XX      gene and sequence encoding (1) and a third sequence encoding a
XX      termination region functional in the host cell and growing the host cell
XX      to produce a fusion polypeptide. The method or (1) is useful for
XX      expression of a thioredoxin or thioredoxin reductase by a host cell. This
XX      sequence encodes a oleosin oil body protein fused to Arabidopsis thaliana
XX      thioredoxin gene controlled by a phaseolin promoter and phaseolin
XX      terminator sequence.
XX
XX      Sequence 3888 BP; 1254 A; 722 C; 613 G; 1299 T; 0 other:
XX
XX      Alignment Scores:
XX      Pred. No.: 1.58e-54 Length: 3888
XX      Score: 485.00 Matches: 89

```


OY	4	SerserGIugluGIuglyInValIIeserCysHsthVrValGIugluTTPAsnAspGlnLeu	23
	
Db	1558	GCTTCGGAAAGGACCAAGATGATCGCCACACCCGTTGGAGACATGGACGACAGCTT	16177
OY	24	GIuIysGGLyasnGlnSerLysLysLeuLeuValValAspPheThrAlaSerTProCysGLY	43
	
Db	1618	CAGAAAGCTAATGAAATCCAAAACHTCTTGGTGGTGAATTCACGGCTCTTGGGTGGGA	16777
OY	44	ProCysArpPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIle	63
	
Db	1678	CCATGTCGCTTCACAGCTCCACATTCCTTCTGCTAATTTGGCTAAGAAACCTCTACAGTGCTT	17377
OY	64	PheLeuLysValAspValAspGlnLeuLysSerValSerGlnAspTPRAlaIIeGluAla	83
	
Db	1738	TTCTTCCAAGGTTGATACTGATGAATTTGAAGTCGGTGGCAGCTGATTTGGGCATPACAGGCG	17977
OY	84	MetProThrPheValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLys	103
	
Db	1798	ATGCCAACCTTCATGCTTTTGAAGGAAGGAAGATTTTGGACAAAGTTGTTGGAGCCAAAG	18577
OY	104	LysAspGlnLeuGlnGlnLysIleGlnLysHisValAlaSerAla	118
	
Db	1858	AAAGATGAGCTTCAGTCTACCATTTGCCAAACACTGGCTATANGCGG	1902
RESULT 4			
AB212358			
ID	AB212358	standard; DNA; 345 bp.	
XX	AB212358;		
AC			
XX			
DT	21-JAN-2003	(first entry)	
DE	Arabidopsis thaliana stress regulated gene SEQ ID NO 163.		
XX			
KW	Arabidopsis thaliana; plant; gene; stress; transgenic; ds.		
XX			

Score:	482.00	Matches:	88
Percent Similarity:	89.38%	Conservative:	133
Best Local Similarity:	77.88%	Mismatches:	12
Query Match:	78.37%	Indels:	0
DB:	24	Gaps:	0

US-09-786-715-6 (1-120) x ABN89587 (1-345)

OY	4	SerSerGIuGIuGIuValIIleSerCySHpHrValGIuGIuTPraAspGIuLeu	23
	4	GCCTGGAGAAAGGACMACTGATCCGCTCCACACCGTTGGACATGAAGACACCTT	63
Db	4	GIuLysGIuAsnGIuSerLysLysLeuIIeValAspPheHrAlaSerTPoCysGIy	43
	64	CAGAAAGCTAAATGAATCCAAACCTCTTGCGGTGATTCACAGCCTCTTGGTGGGA	123
OY	44	ProCysArgPheIIaIaIaProPheLeuIIaGIuLeuIIaLysLysPheHrSerValIIe	63
	124	CCATGTCGTTTATCGCTCCATCTCTTGCTGATTTGGCTAAGAAACTTCCTCAAGTGCCTT	183
Db	64	PheLeuLysValAspValAspGIuLeuLysSerValSerGIuAspTPaIIaIIeGIuAla	83
	184	TTTCCTCAAGGTTGATACGTGATGAATTTGAATCGGTGGCAAGTGTGGCGATACAGCGC	243
OY	84	MetProThrPheValPheValLysGIuGIuHrPheLeuAspLysValIIaGIuAlaLys	103
	244	ATGCCACACTTATGTTTGGAGAAAGGAAAGATTTGGCAAAAGTGTGGAGCCAAAG	303
Db	104	LysAspGIuLeuGIuGIuLysIIeGIuLysHrIIaValAla	116
	304	AAAGATGACCTTCAGTCTACCATTTGCCAAACACTGTGGCT	342

RESULT 6

ID AAC51522 standard; DNA; 561 BP.

AC AAC51522;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 68832.

KW Hybridisation assay; genetic mapping; gene expression control;

KW metabolic pathway; promoter; termination sequence; ss.

05 *Arabidopsis thaliana*.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 09-MAR-1999; 99US-0123548.

PR 25-MAR-1999; 99US-0126264.

PR 01-APR-1999; 99US-0127462.

PR 08-APR-1999; 99US-0128714.

PR 19-APR-1999; 99US-0130077.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132485.

PR	06-MAY-1999	9905-01324287
PR	07-MAY-1999	9905-01324286
PR	11-MAY-1999	9905-01342556
PR	14-MAY-1999	9905-01342418
PR	14-MAY-1999	9905-01342419
PR	14-MAY-1999	9905-01343470
PR	18-MAY-1999	9905-01343471
PR	19-MAY-1999	9905-01347461
PR	20-MAY-1999	9905-01351524
PR	21-MAY-1999	9905-01351523
PR	24-MAY-1999	9905-01356529
PR	25-MAY-1999	9905-01366021
PR	27-MAY-1999	9905-01363692
PR	28-MAY-1999	9905-01367822
PR	01-JUN-1999	9905-01372722
PR	04-JUN-1999	9905-01375728
PR	07-JUN-1999	9905-01375702
PR	08-JUN-1999	9905-01377224
PR	10-JUN-1999	9905-01380694
PR	10-JUN-1999	9905-01385400
PR	14-JUN-1999	9905-01386847
PR	16-JUN-1999	9905-01391512
PR	16-JUN-1999	9905-01394522
PR	17-JUN-1999	9905-01394653
PR	18-JUN-1999	9905-01394692
PR	18-JUN-1999	9905-01394545
PR	18-JUN-1999	9905-01394654
PR	18-JUN-1999	9905-01394655
PR	18-JUN-1999	9905-01394566
PR	18-JUN-1999	9905-01394567
PR	18-JUN-1999	9905-01394660
PR	18-JUN-1999	9905-01394661
PR	18-JUN-1999	9905-01394662
PR	18-JUN-1999	9905-01394663
PR	18-JUN-1999	9905-01397570
PR	18-JUN-1999	9905-01397653
PR	21-JUN-1999	9905-01396177
PR	22-JUN-1999	9905-01396899
PR	22-JUN-1999	9905-01403553
PR	23-JUN-1999	9905-01403554
PR	24-JUN-1999	9905-01406095
PR	28-JUN-1999	9905-01406231
PR	28-JUN-1999	9905-01406921
PR	30-JUN-1999	9905-0141287
PR	01-JUL-1999	9905-01418424
PR	01-JUL-1999	9905-01418425
PR	02-JUL-1999	9905-01420555
PR	06-JUL-1999	9905-01423900
PR	08-JUL-1999	9905-01428203
PR	09-JUL-1999	9905-01428220
PR	12-JUL-1999	9905-01429377
PR	13-JUL-1999	9905-01435324
PR	14-JUL-1999	9905-01435324
PR	15-JUL-1999	9905-01440055
PR	16-JUL-1999	9905-01440805
PR	16-JUL-1999	9905-01440806
PR	19-JUL-1999	9905-01443321
PR	19-JUL-1999	9905-01443321
PR	19-JUL-1999	9905-01443324
PR	19-JUL-1999	9905-01443333
PR	19-JUL-1999	9905-01443334
PR	19-JUL-1999	9905-01443335
PR	20-JUL-1999	9905-01443552
PR	20-JUL-1999	9905-01443552
PR	20-JUL-1999	9905-01443684
PR	21-JUL-1999	9905-01448141
PR	21-JUL-1999	9905-01445064
PR	21-JUL-1999	9905-01450888
PR	22-JUL-1999	9905-01450887
PR	22-JUL-1999	9905-01450885

```

PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147312.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151085.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159283.
PR 13-OCT-1999; 99US-0159284.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.

```

```

PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
Pred. No.: 2,62e-55 Length: 561
Score: 482.00 Matches: 88
Percent Similarity: 89.38% Conservative: 13
Best Local Similarity: 77.88% Mismatches: 12
Query Match: 78.37% Indels: 0
DB: 21 Gaps: 0

US-09-786-715-6 (1-120) x AAC51522 (1-561)
QY 4 SerserGlucIuGIyGlnValIleserCySHisThrValGluIuTrpAsnAspGlnLeu 23
DB 97 GCTTCGAGAAAGACAGCAAGATGATCGCTGCACACCTTGAACATGAGCAAGACACTT 156
QY 24 GlnIySGIyAsnGluSerLysLysLeuIleValValAspPheThrAlaSerTPCyGly 43
DB 157 CAGAGGCTATGATGATCAAAACTCTGTGTGTGATTTCACGCGCTTCTGTGTGGA 216
QY 44 ProcysArpHeIleAlaProPheLeuAlaGlnLeuAlaLysLysPheThrSerValIle 63
DB 217 CCATGTCGTTTCATCGCTCCATCTTGTGTAATTTGGCTAAGAAACTTCTTAACGTGCTT 276
QY 64 PheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAla 83
DB 277 TTCCTCAAGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 336
QY 84 MetProThrPheValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLys 103
DB 337 ATGCCAACCTTTCATGTTTGAAGAGGAAGAAATTTGGACAAGTTGTTGAGCCAG 396
QY 104 LysAspGluLeuGlnGlnLysIleGlnLysHisValAla 116
DB 397 AAGATGAGCTTCATGCTACCATTTGCCAACAACCTTGCT 435

RESULT 7
AAC34121
ID AAC34121. standard; DNA; 563 BP.
XX
AC AAC34121.
XX
XX 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 5524.
XX
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
PD
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.

```

PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 28-APR-1999; 99US-0130891.
 PR 30-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 04-MAY-1999; 99US-0132407.
 PR 05-MAY-1999; 99US-0132484.
 PR 06-MAY-1999; 99US-0132486.
 PR 06-MAY-1999; 99US-0132487.
 PR 07-MAY-1999; 99US-0132863.
 PR 11-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.
 PR 14-MAY-1999; 99US-0134219.
 PR 14-MAY-1999; 99US-0134370.
 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139763.
 PR 21-JUN-1999; 99US-0139817.
 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144352.
 PR 20-JUL-1999; 99US-0144632.
 PR 21-JUL-1999; 99US-0144884.
 PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0156559.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.

```

PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158028.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

```

```

Alignment Scores:
Pred. No.: 2.63e-55      Length: 563
Score: 482.00           Matches: 88
Percent Similarity: 89.38%      Conservative: 13
Best Local Similarity: 77.88%    Mismatches: 12
Query Match: 78.37%           Indels: 0
DB: 21                  Gaps: 0

```

US-09-786-715-6 (1-120) x AAC34121 (1-563)

```

QY 4 SerSerGluGluGlyGlnValIleSerCySHsthrValGluGluTTPAsnAspGlnLeu 23
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 99 GCTTCGGAAGAGACAGATGATGCTGCTCCACACCGTTGAGACATGGAACGACAGCTT 158
   |||||
QY 24 GlnlySgIyAsnGluSerLySlyLeuIleValValAspPheThrAlaSerTrpCysGly 43
   |||||
DB 159 CAGAAAGCTATGATGATCCAAACCTCTTGCGTGTGATTTACAGCGCTTCTTGCGTGA 218
   |||||
QY 44 ProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLySlyPheThrSeryAlle 63
   |||||
DB 219 CCATGTCGTTTCATCGCTCCATCTTCTGATTTGGCTAAGAAACCTTCCTAACGTCCTT 278
   |||||
QY 64 PheIleuysValAspValAspGluLeuysSerValSergInaSPTrpAlaIleGluAla 83
   |||||
DB 279 TTCCCTCAAGGTGATGATGATGAATGATGAGTGGGCAAGTATGGCGATACAGGCG 338
   |||||
QY 84 MetProThrPheValAlaPheValIySgIyThrIleuLeuAspLySlyValAlaIyAlaLyS 103
   |||||
DB 339 ATGCCAACCTTCATGTTTGTGAGAAGGAAGAAATTTGGACAAAGTTGTGGAGCCAG 398
   |||||
QY 104 LysAspGluLeuGlnGlnLySlyIleGlnLyShisValAla 116
   |||||
DB 399 AAGATGAGCTTCAGTCTACCATTCGCCAAACACTTGGCT 437
   |||||

```

```

RESULT 8
ABSS3095
ID ABSS3095 standard; DNA; 3129 BP.
XX
AC ABSS3095;

```

```

XX 29-NOV-2002 (first entry)
DT DNA encoding thioredoxin-phaseolin fusion protein.
DE Thioredoxin; thioredoxin reductase; gene expression; oleosin;
XX oil body; gene; ds; thioredoxin reductase; phaseolin.
KW Arabidopsis thaliana.
XX Phaseolin vulgaris.
OS Synthetic.
OS Key Location/Qualifiers
FH CDS 1555..1899
FT /tag=a
FT /product="Thioredoxin-phaseolin fusion protein"
XX
XX US200208025-A1.
XX
XX 04-JUL-2002.
XX
XX 03-JUL-2001; 2001US-0897425.
XX
XX 22-FEB-1991; 91US-0659835.
XX 16-NOV-1993; 93US-0142418.
XX 30-DEC-1994; 94US-0366783.
XX 25-APR-1997; 97US-0846021.
XX 18-DEC-1998; 98US-0210843.
XX
XX (MOLO/) MOLONEY M. M.
XX (DALM/) DALMIA B. K.
XX
XX Moloney MM, Dalmlia BK;
XX
XX WPI: 2002-635723/68.
XX P-PSDB: ABG32916.
XX
XX Expressing protein, by introducing chimeric nucleotide regulatory
XX sequence, sequence encoding fusion protein, having sequence encoding
XX protein, oleosin gene and sequence encoding termination region and
XX producing protein.
XX
XX Example 21; Fig 12; 69pp; English.
XX
XX The invention describes a method of expressing thioredoxin or thioredoxin
XX reductase (I) in the oil body of a host cell using an oil body protein
XX gene. The method involves introducing a chimeric nucleic acid comprising
XX a first sequence to regulate transcription, a second DNA sequence
XX encoding a fusion polypeptide, comprising a sequence encoding an oleosin
XX gene and sequence encoding (I) and a third sequence encoding a
XX termination region functional in the host cell and growing the host cell
XX to produce a fusion polypeptide. The method or (I) is useful for
XX expression of a thioredoxin or thioredoxin reductase by a host cell. This
XX sequence represents an Arabidopsis thaliana thioredoxin gene controlled
XX by a phaseolin promoter and terminator for use in an expression vector.
XX
XX Sequence 3129 BP; 1051 A; 549 C; 439 G; 1090 T; 0 other;

```

```

Alignment Scores:
Pred. No.: 2.95e-54      Length: 3129
Score: 482.00           Matches: 88
Percent Similarity: 89.38%      Conservative: 13
Best Local Similarity: 77.88%    Mismatches: 12
Query Match: 78.37%           Indels: 0
DB: 24                  Gaps: 0

```

US-09-786-715-6 (1-120) x ABSS3095 (1-3129)

```

QY 4 SerSerGluGluGlyGlnValIleSerCySHsthrValGluGluTTPAsnAspGlnLeu 23
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 1558 GCTTCGGAAGAGACAGATGATGCTGCTCCACACCGTTGAGACATGGAACGACAGCTT 1617
   |||||
QY 24 GlnlySgIyAsnGluSerLySlyLeuIleValValAspPheThrAlaSerTrpCysGly 43
   |||||

```

```

Cc      1618 CAGAAAGCTAATGAAATCAAAACCTTGTGGTGTGATTTCAGCGCTTCTTGCTGGA 1677
Cc      44  ProcyasargPhelelealProPheleuAlaIgluLeuAlaLysLysPhehrSerValIle 63
Cc      1678 CCATGCGCTTTATCCCTCCATCTTGTGATTGGCTAAGAAACCTTCTACCGTGCCT 1737
Cc      64  PheleuLysValasPvalasPgluLeuLysSerValSerGlnasPrralalIlegluAla 83
Cc      1738 TTCCTCAAGCTTGATCTGATCATGATTAAGTCCGCTGCAAGTATTGGCGGATACAGGCC 1797
Cc      84  MetProThrPheValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLys 103
Cc      1798 ATGCCAACCTTCATGTTTGAAGGAAGCAAGATTTTGACAAAGTGTGGAGCCCAAG 1857
Cc      104  LysAspGluLeuGlnGlnLysIleGlnLysHisValAla 116
Cc      1858 AAGATGAGCTTCAGTCACTACCATTTGCCAAACACTTGCGCT 1896
Cc      ABN89579 standard; DNA; 3129 BP.
Cc      ABN89579;
Cc      06-SEP-2002 (first entry)
Cc      Phaseolin promoter-Arabidopsis Trxn-phaseolin terminator DNA SEQ.14.
Cc      Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
Cc      oil body; ophthalmological; antidiabetic; cytosolic; antipsoriatic;
Cc      vasotropic; vulnary; antibacterial; immunosuppressive; antilicer;
Cc      food product; milk; wheat; oxidative stress; cataract; diabetes;
Cc      chronic obstructive pulmonary disease; emvenomation; psoriasis; sepsis;
Cc      bronchopulmonary disease; malignancy; reperfusion injury; wound healing;
Cc      gastro intestinal bleeding; intestinal bowel disease; ulcer;
Cc      gastro oesophageal reflux disease; gene; ds.
Cc      Arabidopsis sp.
Cc      OS Phaseolus vulgaris.
Cc      PN WO200250289-A1.
Cc      PD 27-JUN-2002.
Cc      PF 19-DEC-2001: 2001MO-US50240.
Cc      PR 19-DEC-2000: 2000US-0742900.
Cc      PR 05-JUL-2001: 2001US-30285P.
Cc      PR 04-DEC-2001: 2001US-0006038.
Cc      PA (SEMB-) SEMBIOSYS GENETICS INC.
Cc      PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Cc      PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
Cc      PI Del Val G, Zaplachinski S, Moloney M;
Cc      XX MPI: 2002-508806/54.
Cc      DR P-PSDB; ABP60680.
Cc      XX Producing oil body associated with recombinant multimeric protein
Cc      PT complex e.g. redox proteins and immunoglobulins comprises producing
Cc      PT recombinant polypeptides capable of forming the complex in cells
Cc      PT comprising oil bodies -
Cc      XX Example 2; Page 165-166; 362pp; English.
Cc      The present invention describes a method (M1) for producing an oil body
Cc      CC associated with a recombinant multimeric protein complex (MPC). M1
Cc      CC comprises producing in a cell comprising oil bodies a first and second
Cc      CC recombinant polypeptide (P1, P2), where P1 is capable of associating
Cc      CC with P2 to form the MPC and associating the complex with an occlusion
Cc      CC body (OB) through an OB-targeting-protein capable of associating with OB

```

```

Cc      and P1. M1 is useful for producing an oil body associated with a
Cc      CC recombinant MPC. The oil bodies are further formulated for use in the
Cc      CC preparation of a food product such as milk or wheat based food product,
Cc      CC personal care product which reduces the oxidative stress on the surface
Cc      CC area of the human body or used to lighten the skin, or a pharmaceutical
Cc      CC composition used to treat chronic obstructive pulmonary disease (COPD),
Cc      CC cataracts, diabetes, emvenomation, bronchopulmonary disease, psoriasis,
Cc      CC malignancies, reperfusion injury, wound healing, sepsis, gastro
Cc      CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
Cc      CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677
Cc      CC to ABP60964 represent sequence given in the exemplification of the
Cc      CC present invention.
Cc      SQ Sequence 3129 BP; 1051 A; 549 C; 439 G; 1090 T; 0 other;
Cc      Alignment Scores:
Cc      Pred. No.: 2.95e-54 Length: 3129
Cc      Score: 482.00 Matches: 88
Cc      Percent Similarity: 89.38% Conservative: 13
Cc      Best Local Similarity: 77.88% Mismatches: 12
Cc      Query Match: 78.37% Indels: 0
Cc      DB: 24 Gaps: 0
Cc      US-09-786-715-6 (1-120) x ABN89579 (1-3129)
Cc      QY 4 SerSerGluGluGlyInValIleSerCySHisThrValGluGluTrpAsnAspGlnLeu 23
Cc      DB 1558 GCTTCGGAGACAGGACAGAGATGATCGCTGCCACACCGTTGACGATGAGACGACGCTT 1617
Cc      QY 24 GlnLysGlyAsnGlnSerLysLysLeuIleValValasPhehrAlaSerTrpCysGly 43
Cc      DB 1618 CAGAAAGCTAATGAAATCAAAACCTTGTGGTGTGATTTCAGCGCTTCTTGCTGGA 1677
Cc      QY 44 ProcyasargPhelelealProPheleuAlaIgluLeuAlaLysLysPhehrSerValIle 63
Cc      DB 1678 CCATGCGCTTTATCCCTCCATCTTGTGATTGGCTAAGAAACCTTCTACCGTGCCT 1737
Cc      QY 64 PheleuLysValasPvalasPgluLeuLysSerValSerGlnasPrralalIlegluAla 83
Cc      DB 1738 TTCCTCAAGCTTGATCTGATCATGATTAAGTCCGCTGCAAGTATTGGCGGATACAGGCC 1797
Cc      QY 84 MetProThrPheValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLys 103
Cc      DB 1798 ATGCCAACCTTCATGTTTGAAGGAAGCAAGATTTTGACAAAGTGTGGAGCCCAAG 1857
Cc      QY 64 PheleuLysValasPvalasPgluLeuLysSerValSerGlnasPrralalIlegluAla 83
Cc      DB 1738 TTCCTCAAGCTTGATCTGATCATGATTAAGTCCGCTGCAAGTATTGGCGGATACAGGCC 1797
Cc      QY 84 MetProThrPheValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLys 103
Cc      DB 1798 ATGCCAACCTTCATGTTTGAAGGAAGCAAGATTTTGACAAAGTGTGGAGCCCAAG 1857
Cc      QY 104 LysAspGluLeuGlnGlnLysIleGlnLysHisValAla 116
Cc      DB 1858 AAGATGAGCTTCAGTCACTACCATTTGCCAAACACTTGCGCT 1896
Cc      RESULT 10
Cc      ABS53096
Cc      ID ABS53096 standard; DNA; 3888 BP.
Cc      AC ABS53096;
Cc      XX 29-NOV-2002 (first entry)
Cc      DE DNA encoding Oleosin-thioredoxin fusion protein.
Cc      XX Thioredoxin; thioredoxin reductase; gene expression; oleosin;
Cc      KW oil body; oleosin-thioredoxin fusion protein; gene; ds.
Cc      XX Arabidopsis thaliana.
Cc      OS Brassica napus.
Cc      OS Synthetic.
Cc      OS XX
Cc      FH Key Location/Qualifiers
Cc      FT CDS 1555..2658
Cc      FT /*tag= a
Cc      FT /*product= "Oleosin-thioredoxin fusion protein"
Cc      FT 1555..1907
Cc      FT /*tag= b
Cc      FT /*number= 1

```

```
FT intron 1908..2147
FT /*tag= c
FT /number= 1
FT exon 2148..2658
FT /*tag= d
FT /number= 2
XX
XX US2002088025-A1.
XX
XX 04-JUL-2002.
XX
XX 03-JUL-2001; 2001US-0897425.
XX
XX 22-FEB-1991; 91US-0659835.
XX 16-NOV-1993; 93US-0142418.
XX 30-DEC-1994; 94US-0366783.
XX 25-APR-1997; 97US-0846021.
XX 18-DEC-1998; 98US-0210843.
XX
XX (MOLO/) MOLONEY M M.
XX (DALM/) DALMIA B K.
XX
XX Moloney KM, Dalmia BK;
XX
XX WPI: 2002-635723/68.
XX P-PSDB: AB632917.
XX
XX Expressing protein, by introducing chimeric nucleotide regulatory
XX sequence, sequence encoding fusion protein, having sequence encoding
XX protein, oleosin gene and sequence encoding termination region and
XX producing protein
XX
XX Example 21: Fig 13; 69pp: English.
XX
XX The invention describes a method of expressing thioredoxin or thioredoxin
XX reductase (I) in the oil body of a host cell using an oil body protein
XX gene. The method involves introducing a chimeric nucleic acid comprising
XX a first sequence to regulate transcription, a second DNA sequence
XX encoding a fusion polypeptide, comprising a sequence encoding an oleosin
XX gene and sequence encoding (I) and a third sequence encoding a
XX termination region functional in the host cell and growing the host cell
XX to produce a fusion polypeptide. The method or (I) is useful for
XX expression of a thioredoxin or thioredoxin reductase by a host cell. This
XX sequence encodes a oleosin oil body protein fused to Arabidopsis thaliana
XX thioredoxin gene controlled by a phaseolin promoter and phaseolin
XX terminator sequence.
XX
XX Sequence 3888 BP; 1254 A; 723 C; 613 G; 1298 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 4,01e-54 Length: 3888
Score: 482.00 Matches: 88
Percent Similarity: 89.38% Conservatave: 13
Best Local Similarity: 77.88% Mismatches: 12
Query Match: 78.37% Indels: 0
DB: 24 Gaps: 0
US-09-786-715-6 (1-120) x ABS53096 (1-3888)
QY 4 SerSerGluGluGluGluValIleSerGlySHSThrValIleGluGluTrpAsnAspGluLeu 23
DB 2317 GCTTCGGAAGAGGACAGTATCGCCGACACACCGTTGAGACATGGAGACGACGACTT 2376
QY 24 GlnTyrGluAsnGluSerLysLysLeuIleValIleAspPheThrAlaSerTrpCysGly 43
DB 2377 CAGAAAGCTATGATCAATCAAAACCTTGTGTGGTGTGATTTCACGCGCTTTCGTGTGGA 2436
QY 44 ProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIle 63
DB 2437 CCATGTCGTTTCATTCGTCATTCCTTTCGATTTGGCTAGAAACCTTCCTAAGCGTCTT 2496
QY 64 PheLeuGluValAspValAspGluLeuLysSerValSerValSerGluAspTrpAlaIleGluAla 83
```

```
DB 2497 TTCCTCAAGCTTGATGATGATGAATTGAAGTCGTGGCAAGTATGGCGCATACAGCGC 2556
QY 84 MetProThrPheValPheValLysGluGluThrLeuLeuAspLysValValGlyValLys 103
DB 2557 ATGCCACCTTCATGTGTTTGGAGGAGGAGAGATTTTGGACAAAGTTGTTGGAGCCAA 2616
QY 104 LysAspGluLeuGluGlnLysIleGlnLysHisValAla 116
DB 2617 AAGATGAGCTTCAGTCTACATTCACATTCGCAACACTGGCT 2655
RESULT 11
ABN89580
ID ABN89580 standard; DNA; 3888 BP.
XX
XX ABN89580;
XX
XX 06-SEP-2002 (first entry)
XX
XX Phaseolin promoter-oleosin Trxh-phaseolin terminator DNA SEQ:16.
XX
XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
XX oil body; ophthalmological; antidiabetic; cytotatic; antipsoriatic;
XX vasotropic; vulnary; antibacterial; immunosuppressive; antilecer;
XX food product; milk; wheat; oxidative stress; cataract; diabetes;
XX chronic obstructive pulmonary disease; emvenomation; psoriasis; sepsis;
XX bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
XX gastro intestinal bleeding; intestinal bowel disease; ulcer;
XX gastro oesophageal reflux disease; gene; ds.
XX
XX Arabidopsis SP.
XX Phaseolus vulgaris.
XX
XX WO200250289-A1.
XX
XX 27-JUN-2002.
XX
XX 19-DEC-2001; 2001WO-US50240.
XX
XX 19-DEC-2000; 2000US-0742900.
XX 05-JUL-2001; 2001US-302885P.
XX 04-DEC-2001; 2001US-0006038.
XX
XX (SEMB-) SEMBIOSYS GENETICS INC.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
XX Del Val G, Zaplachinski S, Moloney M;
XX
XX WPI: 2002-508806/54.
XX P-PSDB: ABP60681.
XX
XX Producing oil body associated with recombinant multimeric protein
XX complex e.g. redox proteins and immunoglobulins comprises producing
XX recombinant polypeptides capable of forming the complex in cells
XX comprising oil bodies
XX
XX Example 2: Page 167-168; 362pp: English.
XX
XX The present invention describes a method (M1) for producing an oil body
XX associated with a recombinant multimeric protein complex (MPC). M1
XX comprises producing in a cell comprising oil bodies a first and second
XX recombinant polypeptide (P1, P2), where P1 is capable of associating
XX with P2 to form the MPC and associating the complex with an occlusion
XX body (OB) through an OB-targeting-protein capable of associating with OB
XX and P1. M1 is useful for producing an oil body associated with a
XX recombinant MPC. The oil bodies are further formulated for use in the
XX preparation of a food product such as milk or wheat based food product,
XX personal care product which reduces the oxidative stress on the surface
XX area of the human body or used to lighten the skin, or a pharmaceutical
XX composition used to treat chronic obstructive pulmonary disease (COPD),
XX cataracts, diabetes, emvenomation, bronchiopulmonary disease, psoriasis,
XX malignancies, reperfusion injury, wound healing, sepsis, gastro
XX intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
```


PR 16-APR-1999; 99US-0129845.

```

PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.

```

```

PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
Pred. No.: 7.06e-55
Score: 478.00
Percent Similarity: 89.29%
Best Local Similarity: 77.68%
Query Match: 77.72%
DB: 21
Gaps: 0

US-09-786-715-6 (1-120) x AAC37781 (1-470)

QY 4 SerSergIugIugIyGInValIIleSerCySHsthrValIglIugIuTPAsnAspGluLeu 23
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 98 GCTTGGAGAGAGACAGTATGTCGCCACACCGTTGAGACATGGACAGCAGCTT 157
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

QY 24 GlnLysgIAsngIuSerLysLysLeuIleValValAspPheThrAlaSerTrpCysGly 43
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 158 CAGAAAGCCTATGATGATCAAAACCTTGTGTGTTGATTCACGGCTTCTTGATGGA 217
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

QY 44 ProCysArgPheIleAlaProPheLeuAlaLeuAlaLysLysPheThrSerValIle 63
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 218 CCATGTCGTTCAATGCCATCTCTTGCATTTGGCTAGAAACTTCCTCAAGCTCTT 277
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

QY 64 PheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAla 83
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 278 TTCCTCAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 337
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

QY 84 MetProThrPheValIlePheValLysGluGlyThrLeuLeuAspLysValValIleGlyAlaLys 103
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 338 ATGCCAACCTTCATGCTTTTGAAGAGAGAGAAATTTGGCAAAAGTTGTTGAGCCAG 397
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

QY 104 LysAspGluLeuGlnGlnLysIleGlnLysHisVal 115
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB 398 AAGATGAGCTTCAGTCTACCATTCGCCAAACACTTG 433
   ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

RESULT 13
ABN89586 standard; DNA; 4935 BP.
ID ABN89586
AC ABN89586;
XX
XX
XX 06-SEP-2002 (first entry)
DT
XX
XX
DE Promoter-Oleosin thioredoxin reductase-linker-thioredoxin-terminator #33.
XX
XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
KW oil body; ophthalmological; antidiabetic; cytostatic; antiporiatic;
KW vasotropic; vulnerary; antibacterial; immunosuppressive; antiulcer;
KW food product; milk; wheat; oxidative stress; cataract; diabetes;
KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;

```

KW bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KW gastro oesophageal reflux disease; gene; ds.
 XX
 OS Arabidopsis sp.
 OS Phaseolus vulgaris.
 PN WO200250289-A1.
 XX
 XX 27-JUN-2002.
 XX
 PF 19-DEC-2001; 2001WO-US50240.
 XX
 PR 19-DEC-2000; 2000US-0742900.
 PR 05-JUL-2001; 2001US-302885P.
 PR 04-DEC-2001; 2001US-0006038.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 DR WPI; 2002-508806/54.
 DR P-PSDB; ABP60692.
 XX
 PT Producing oil body associated with recombinant multimeric protein
 PT complex e.g. redox proteins and immunoglobulins comprises producing
 PT recombinant polypeptides capable of forming the complex in cells
 PT comprising oil bodies -
 XX
 XX Example 2; Page 189-192; 362pp; English.
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating
 CC with P2 to form the MPC and associating the complex with an occlusion
 CC body (OB) through an OB-targeting-protein capable of associating with OB
 CC and P1. M1 is useful for producing an oil body associated with a
 CC recombinant MPC. The oil bodies are further formulated for use in the
 CC preparation of a food product such as milk or wheat based food product,
 CC personal care product which reduces the oxidative stress on the surface-
 CC area of the human body or used to lighten the skin, or a pharmaceutical
 CC composition used to treat chronic obstructive pulmonary disease (COPD),
 CC cataracts, diabetes, envenomation, bronchiolopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677
 CC to ABP60964 represent sequence given in the exemplification of the
 CC present invention.
 XX
 XX Sequence 4935 BP; 1528 A; 932 C; 898 G; 1577 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 2 64e-53 Length: 4935
 Score: 477.00 Matches: 87
 Percent Similarity: 89.19% Conservative: 12
 Best Local Similarity: 78.38% Mismatches: 12
 Query Match: 77.56% Indels: 0
 DB: 24 Gaps: 0
 US-09-786-715-6 (1-120) x ABN89586 (1-4935)
 OY 6 GluGluGluGluValIleSerGlyShrValGluGluTrpAsnAspGlnLeuGlnLys 25
 Db 3369 GAAAGAGGACAGTGTATCCCTGCCACACGTTGAGACATGGAACAGACAGCTTCAGAG 3428.
 OY 26 GlyAsnGluSerLysLysLeuIleValIleAspPheThrAlaSerTrpCysGlyProCys 45
 Db 3429 GCTAATGAATCCAAACCTCTGTGGTGTGATTTCACGCGCTTGTGGTGGACATGT 3488
 OY 46 ArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSerValIlePheLeu 65

Db 3489 CGTTTCATGCGTCCATCTTCTGCTGATTTGGCTAAGAACTCCATACGCTTTTCCTC 3548
 OY 66 LysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIleGluAlaMetPro 65
 Db 3549 AAGGTGATACATGATGAATTTGAAGTGGTGGCAAGTATGGCGGATACAGGCCA 3608
 OY 86 ThrPheValPheValLysGluGlyThrLeuLeuAspLysValValGlyAlaLysLysAsp 105
 Db 3609 ACCTTCATGTTTGTGAGCAAGGAGGATTTTGACAAAGTTGTGTGGACCAAGAACAT 3668
 OY 106 GluLeuGluGluLysIleGlnLysHisValAla 116
 Db 3669 GAGCTTCAGCTACCATTCGCAACACACTTGCT 3701
 RESULT 14
 AAH87768
 ID AAH87768 standard; cDNA; 509 BP.
 XX
 AC AAH87768;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Peppermint plant oil gland expressed cDNA 124.
 XX
 KW Peppermint; plant oil gland cell; terpenoid essential oil; resin;
 KW genetic mapping; antisense suppression; recombinant expression; ss.
 OS Mentha x piperita.
 XX
 PN WO200153319-A1.
 XX
 PD 26-JUL-2001.
 PF 19-JAN-2001; 2001WO-US02567.
 PR 20-JAN-2000; 2000US-0177264.
 XX
 PA (CROT/) CROTEAU R. B.
 PA (LANGE/) LANGE B M.
 PA (WILD/) WILDUNG M R.
 XX
 PI Croteau RB, Lange BM, Wildung MR;
 DR WPI; 2001-488706/53.
 XX
 PT New nucleic acid molecules corresponding to mRNA molecules expressed in
 PT peppermint oil glands for enhancing expression of plant oil gland cell
 PT proteins -
 XX
 PS Claim 1; Page 125; 251pp; English.
 XX
 CC The invention relates to nucleic acid molecules (AAH87645-AAH88116) that
 CC correspond to all or part of a mRNA molecule expressed in plant oil
 CC gland cells, especially peppermint and plant oil glands that produce
 CC terpenoid essential oils and resins. The nucleic acids are useful for
 CC genetically mapping a plant genome for genes expressed in plant oil
 CC gland cells and to suppress (for example by antisense suppression) or
 CC enhance their expression (for example by genetically transforming a
 CC plant cell with a replicable expression vector that expresses one or more
 CC proteins naturally expressed in plant oil gland cells). The nucleic acids
 CC are also useful for recombinant expression of plant oil gland proteins
 CC required for terpenoid essential oil and/or resin production in bacterial
 CC and/or yeast cells.
 XX
 SQ Sequence 509 BP; 144 A; 103 C; 129 G; 133 T; 0 other;
 Alignment Scores:
 Pred. No.: 5.08e-54 Length: 509
 Score: 472.00 Matches: 87
 Percent Similarity: 85.95% Conservative: 17
 Best Local Similarity: 71.90% Mismatches: 16
 Query Match: 76.75% Indels: 1

DB: 22 Gaps: 0

US-09-786-715-6 (1-120) x AAH87768 (1-509)

QY 1 MetIaGlySerSerGluGluGlnValIleSerCysHsIthrValGluGluTrpAsn 20

DB 32 ATGGCTTCGTCGGAATCTGAAGAGAGATCGGCTGCCACCATCGATACCTGGGAC 91

QY 21 AspGlnLeuGlnLysGlnGluSerLysLysLeuIleValIleAspPheThrAlaSer 40

DB 92 GAGCAGCTTCAGAGGGAATGATACAGAGAGAGTTGGAGTTGGATTTCATCTGCC 151

QY 41 TrpCysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThr 60

DB 152 TGGTGGCGGCTTCGCTTCATCGCCCTTTCCTCCAGAAATGGCCAAAGATTCCT 211

QY 61 SerValIlePheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAla 80

DB 212 AATGTGACATTTCTCAAGGTGATGTCAGTGAAGTGGTTGCTAGTGGAGCA 271

QY 81 IleGluAlaMetProThrPheValIleValLysGluGlnLysThrLeuLeuAspLysValIle 100

DB 272 GTGGAGGCAATGCCAACCTTCATCTCTCAAGAGAGAGAGATCTTCGACAGCTGCTA 331

QY 101 -GlyAlaLysLysAspGluLeuGlnLysIleGlnLysHisValAlaSerAlaSerAl 120

DB 332 GGGAGCGCAAGAAAGAGAGAGCTGCAGCAAAATATTGTAAGCAGCTCAACACAGCTACTAG 391

QY 120 a 120

DB 392 T 392

RESULT 15

AA09783 ID AA09783 standard; DNA: 653 BP.

XX AA09783;

AC 24-JUN-1996 (first entry)

XX

DE Plant SAR gene pl.4.3.

XX

KM SAR; tobacco; protein-synthesis independent gene; cycloheximide;

KM systemic acquired resistance response; pl.4.3; anti-pathogen;

XX plant protection; ss.

XX Nicotiana acuminata.

OS

XX W09519443-A2.

PN

XX 20-JUL-1995.

PD

XX 03-JAN-1995; 95MO-1B00002.

PF

XX 13-JAN-1994; 94US-0181271.

PR

XX (CIBA) CIBA GEIGY AG.

PA

XX Alexander DC, Ryals JA, Uknes SJ, Ward ER;

PI

XX MPI; 1995-263872/34.

DR

XX

XX New DNA contg. plant systemic acquired resistance genes - and

PT transgenic plants contg. them, impart disease and pest resistance,

PT also Arabidopsis gene promoter to control DNA transcription

XX

PS Disclosure; Page 61; 85pp; English.

XX

CC This sequence represents the DNA sequence of a tobacco protein-synthesis

CC independent gene. The gene is involved in the regulation of the

CC systemic acquired resistance (SAR) response. This gene is designated

CC pl.4.3. This sequence and AA09784 represent SAR genes that are not used

CC in the recombinant/chimeric DNA molecules of the invention.

CC AA09784-099790 and AA099806 are SAR genes used in the

CC recombinant/chimeric DNA molecules of the invention. The wild type

CC genes corresponding to these sequences can all be chemically induced in a

CC plant in a protein-synthesis independent manner. SAR genes are involved

CC in the protection of plants against pests and disease. These sequences

CC were isolated by differential screening of a cDNA library, followed by

CC analysis by Northern hybridisation to RNA in the presence and absence of

CC cycloheximide. The genes are used in the creation of transgenic plants.

CC Transgenic expression of 2 or more of the recombinant molecules of the

CC invention that encode anti-pathogenic proteins provides a synergistic

CC increase in plant protection, and may also offer protection against a

CC wider range of pathogens.

XX

SQ Sequence 653 BP; 165 A; 114 C; 157 G; 215 T; 2 other;

Alignment Scores:

Pred. No.: 3.13e-50 Length: 653

Score: 445.00 Matches: 84

Percent Similarity: 84.87% Conservative: 17

Best Local Similarity: 70.59% Mismatches: 17

Query Match: 72.36% Indels: 1

DB: 16 Gaps: 0

US-09-786-715-6 (1-120) x AA09783 (1-653)

QY 2 AlaGlySerSerGluGluGlnValIleSerCysHsIthrValGluGluTrpAsn 21

DB 63 GCTACTTCATCCGAGGAGGAGCAAGTGTTCGGCTGCCCAAGGTGAGCAATGCAAGAG 122

QY 22 GlnLeuGlnLysGlnGluSerLysLysLeuIleValValAspPheThrAlaSer 41

DB 123 TACTTCAAGAAAGCGCTTGAGACTAAGAAACTGCTGGTGCATTTTACTGCTTCAATG 182

QY 42 CysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSer 61

DB 183 TGGGSCCTTGCCTTTATTGCCCCAATTTCTCTGACATTCGTAAGAGATGCCCAT 242

QY 62 ValIlePheLeuLysValAspValAspGluLeuLysSerValSer-GlnAspTrpAlaI 81

DB 243 GTTATATTCCTCAAGGTGATGCTGATGCACTGAAAGACTGTTTCAGCGGAGATGAGTGT 302

QY 81 eGluAlaMetProThrPheValIleValLysGluGlnLysThrLeuLeuAspLysValIle 101

DB 303 GAGGCAATGCCCAACTTTTCTTCATTAAGATGAAAGAGTGGACAGAGATGTTGG 362

QY 101 ValAlaLysLysAspGluLeuGlnLysIleGlnLysHisValAlaSerAlaSer 119

DB 363 TGGCAAGAAAGAGAGGTTGACAGCAGCAATGATGATGCTGCTCTGCTACT 417

Search completed: August 17, 2003, 19:37:14

Job time : 173.696 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n-model

Run on: August 17, 2003, 19:18:57 ; Search time 44.472 Seconds
(without alignments)
1190.995 Million cell updates/sec

Title: US-09-786-715-6
Perfect score: 615
Sequence: 1 MAGSSEGGVICHIVEMN.....GAKKDELQKIKHVASASA 120

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 segs, 220691566 residues
Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame-p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool/US09786715/rnat_11082003_150515_6083/app_query.fasta_1.1052
-DB=Issued_Patents.NA -QFMT=fastap -SUFFIX=tni -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cdi
-LIST=45 -DOCALL=0 -NORM=pct -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -COMP=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09786715.ecgn_1_1175.etrnat_11082003_150515_6083 -NCP=6 -ICP=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Issued_Patents.NA:*
2: /cgn2_6/ptodata/1/ina/5a.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5b.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6a.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6b.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	445	72.4	653	1	US-08-181-271A-103
2	445	72.4	653	1	US-08-449-315-103
3	445	72.4	653	1	US-08-444-803-103
4	445	72.4	653	1	US-08-449-043-103
5	445	72.4	653	1	US-08-456-265A-103
6	445	72.4	653	1	US-08-455-416-103
7	445	72.4	653	1	US-08-455-244-103
8	445	72.4	653	1	US-08-454-876-103
9	445	72.4	653	2	US-08-457-364-103
10	445	72.4	653	2	US-08-456-262-103
11	445	72.4	653	2	US-08-456-240-103
12	445	72.4	653	2	US-08-455-736-103

13	445	72.4	653	2	US-08-971-217-103
14	445	72.4	653	3	US-09-350-600-103
15	368	59.8	393	4	US-09-540-014-5
16	367	59.7	382	4	US-09-540-014-3
17	361	58.7	359	4	US-09-540-014-1
18	244.5	39.8	318	4	US-09-313-294A-5868
19	222	36.1	557	4	US-09-404-879A-88
20	222	36.1	557	4	US-09-338-933-88
21	222	36.1	557	4	US-09-338-933-88
22	222	36.1	557	4	US-09-215-681-88
23	222	36.1	581	4	US-09-601-144-67
24	222	36.1	594	4	US-09-404-879A-87
25	222	36.1	594	4	US-09-338-933-87
26	222	36.1	594	4	US-09-215-681-87
27	222	36.1	601	4	US-09-404-879A-133
28	222	36.1	601	4	US-09-338-933-133
29	222	36.1	601	4	US-09-215-681-133
30	222	36.1	624	3	US-09-385-982-526
31	222	36.1	630	3	US-08-180-371-5
32	222	36.1	630	3	US-08-180-371-17
33	211	34.3	605	3	PCT-US92-05707-5
34	203	33.0	631	3	US-09-385-982-485
35	199	32.4	278	4	US-09-313-294A-5840
36	195.5	31.8	914	1	US-08-386-729A-9
37	182.5	29.7	339	4	US-09-107-532A-3085
38	178.5	29.0	336	4	US-09-134-001C-1022
39	173	28.1	564	2	US-08-775-878-2
40	171	27.8	7096	4	US-09-221-017B-373
41	170.5	27.7	1230025	4	US-09-198-452A-1
42	163.5	26.6	4403765	3	US-09-103-840A-2
43	163.5	26.6	4411529	3	US-09-103-840A-1
44	159	25.9	1830121	4	US-09-557-884-1
45	159	25.9	1830121	4	US-09-643-990A-1

ALIGNMENTS

RESULT 1
US-08-181-271A-103
Sequence 103, Application US/08181271A
Patent No. 5614395
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/181,271A
  FILING DATE: 13-JAN-94
  CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/093,301
    FILING DATE: 16-JUL-1993
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/937,197
      FILING DATE: 6-NOV-1992
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 07/678,378
        FILING DATE: 1-APR-1991
        PRIOR APPLICATION DATA:
          APPLICATION NUMBER: US 07/305,566
          FILING DATE: 6-FEB-1989
          PRIOR APPLICATION DATA:
            APPLICATION NUMBER: US 07/165,667
            FILING DATE: 8-MAR-1988
            PRIOR APPLICATION DATA:
              APPLICATION NUMBER: US 08/042,847
              FILING DATE: 6-APR-1993
              PRIOR APPLICATION DATA:
                APPLICATION NUMBER: US 07/632,441
                FILING DATE: 21-DEC-1990
                PRIOR APPLICATION DATA:
                  APPLICATION NUMBER: US 07/425,504
                  FILING DATE: 20-OCT-1989
                  PRIOR APPLICATION DATA:
                    APPLICATION NUMBER: US 07/848,506
                    FILING DATE: 6-MAR-1992
                    PRIOR APPLICATION DATA:
                      APPLICATION NUMBER: US 07/768,122
                      FILING DATE: 27-SEP-1991
                      PRIOR APPLICATION DATA:
                        APPLICATION NUMBER: US 07/580,431
                        FILING DATE: 7-SEP-1990
                        PRIOR APPLICATION DATA:
                          APPLICATION NUMBER: US 07/368,672
                          FILING DATE: 20-JUN-1989
                          PRIOR APPLICATION DATA:
                            APPLICATION NUMBER: US 07/329,018
                            FILING DATE: 24-MAR-1989
                            PRIOR APPLICATION DATA:
                              APPLICATION NUMBER: US 08/045,957
                              FILING DATE: 12-APR-1993
                              ATTORNEY/AGENT INFORMATION:
                                NAME: Elmer, James Scott
                                REGISTRATION NUMBER: 36,129
                                REFERENCE/DOCKET NUMBER: S-19825/P1/GC 1727
                                TELECOMMUNICATION INFORMATION:
                                  TELEPHONE: (919)541-8614
                                  TELEFAX: (919)541-8689
                                INFORMATION FOR SEQ ID NO: 103:
                                  SEQUENCE CHARACTERISTICS:
                                    LENGTH: 653 base pairs
                                    TYPE: nucleic acid
                                    STRANDEDNESS: single
                                    TOPOLOGY: linear
                                  MOLECULE TYPE: DNA (genomic)
                                  US-08-181-271A-103

Alignment Scores:
Pred. No.: 1,68e-54 Length: 653
Score: 445.00 Matches: 84
Percent Similarity: 84.87% Conservative: 17
Best Local Similarity: 70.59% Mismatches: 17
Query Match: 72.36% Indels: 1
DB: 1 Gaps: 0

US-09-786-715-6 (1-120) x US-08-181-271A-103 (1-653)

```

```

QY 2 AlaGlySerSerGluGluGlyGlnValIleSerCysHisThrValGluGluTrpAsnAsp 21
Db 63 GCTACTGATCCGAGAGGAGGACAAAGTTCGGCTGCACAAAGGTTGAGAAATGCAACGAG 122
QY 22 GlnLeuGlnLysGlyAsnGluSerLysLysLeuIleValValAspPheThrAlaSerTrp 41
Db 123 TACTTCAGAAAGCGGTGAGACTAAGAACTGGGTGGTGGATTACTTACTTCATCAGG 182
QY 42 CysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSer 61
Db 183 TGGCGSCCTTCCGCTTTATTTCGCCCATTTCTTCTGTGACATTGCTCAAAAGATGCCCAT 242
QY 62 ValIlePheLeuLysValAspValAspLysLysSerValSer-GlnAspTPPALaI 81
Db 243 GTTATATTCCTCAAGGTGATGTGATGACTGAAGACTGTTTCACCGGAATGAGTGT 302
QY 81 eGluAlaMetProThrPheValPheValLysGluGlyThrLeuLeuAspLysValValG 101
Db 303 GGAGCAATGCCCACTTTTGTCTTCATTAAAGATGAAAGAAAGAGTGCACAGATTGTTGG 362
QY 101 YAlaLysLysAspGluLeuGlnLysIleGlnLysHisValAlaSer 119
Db 363 TGCCAAAGAAAGAGGAGTTGCAGACACCATAGTGAAAGCATGCTCTCTGCTACT 417

RESULT 2
US-08-449-315-103
; Sequence 103, Application US/08449315
; Patent No. 5650505
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,315
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271
; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8614
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-449-315-103
Alignment Scores:
Pred. No.: 1,68e-54 Length: 653
Score: 445.00 Matches: 84
Percent Similarity: 84.87% Conservative: 17
Best Local Similarity: 70.59% Mismatches: 17
Query Match: 72.36% Indels: 1
DB: 1 Gaps: 0
US-09-786-715-6 (1-120) x US-08-449-315-103 (1-653)
QY 2 AlaGlySerSerGluGluGlyGluValIleSerGlyHisThrValGluGluTrpAsp 21
DB 63 GCTACTTCATCCGAGAGGACCAAGTGTTCGGCTGCCACCAAGTTGAGAGAAAGACGAG 122
QY 22 GlnLeuGlnLysGlyAsnGlySerLysLysLeuIleValIleValAspPheThrAlaSerTrp 41
DB 123 TACTTCAGAGAAAGCGCTGAGAGCTAGAAACTGCTGCTGATTTACTCTCTCATGG 182
QY 42 CysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSer 61
DB 183 TCGGSCCTTCGCCGTTTATTGCCCCCAATTCCTGCTGACATTCCTAAGAAAGATGCCCAT 242

QY 62 ValIlePheLeuLysValAspValAspGluLeuLysSerValSer-GlnAspTrpAlaIle 81
DB 243 GTTATATTCCTCAGAGGTGATGTGTGATGACGTAAGACTGTTTACCGGGAAATGAGGTGT 302
QY 81 eGluAlaMetProThrPheValIlePheValLysGluGlyTrpThrLeuLeuAspLysValVal1 101
DB 303 GGAGCAATGCCAAGCTTTGCTCTTCATTAAGATGAAAAGAGTGCAGACAGAGTGTCTTG 362
QY 101 ValAlaLysLysAspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSer 119
DB 363 TCCCAAGAAAGAGAGGATTCACAGACACCATTAAGTGAAGCATGCTGCTCCTGCTACT 417
RESULT 3
US-08-444-803-103
Sequence 103, Application US/08444803
Patent No. 5654414
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesting, John H.
APPLICANT: Friedlich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, SheriLeca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,803
CLASSIFICATION: 536
FILING DATE: 19-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847

LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-456-265A-103

Alignment Scores:
Pred. No.: 1,68e-54 Length: 653
Score: 445.00 Matches: 84
Percent Similarity: 84.87% Conservative: 17
Best Local Similarity: 70.59% Mismatches: 17
Query Match: 72.36% Indels: 1
Gaps: 0

US-09-786-715-6 (1-120) x US-08-456-265A-103 (1-653)

QY 2 AAlaGlySerSerGluGluGluGluValIleSerCysHisThrValGluGluTrpAsnAsp 21
Db 63 GCTACTTCATCCGAGGAGGAGCAAGTTCGCGCCAGCAAGGTTGAGAAATGGAACACAG 122
QY 22 GlnLeuGlnLysGlyAsnGlnSerLysLysLeuIleValValAspPheThrAlaSerTrp 41
Db 123 TACTTCAGAAAGGCGTTGAGACTAAGAACTGGTGGTGCATTTTACTGCTTCATGG 182
QY 42 CysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSer 61
Db 183 TGGGSCCTTGGCGTTTATGCCCCCAATCTTGCTGACATGCTAAGAAAGATGCCCAT 242
QY 62 ValIlePheLeuLysValAspValAspGluLeuLysSerValSer-GlnAspTrpAlaIle 81
Db 243 GTTATATTCCTCAAGGTGTGATGTGATGAACTGTAAGCGGCAATGAGTCT 302
QY 81 eGluAlaMetProThrPheValPheValIleValLysGluGlyThrLeuLeuAspLysValAlaG 101
Db 303 GGAGGCAATGCCACTTTTGTCTCATTAAGATGAAANAAGTGGACAGATGTTGG 362
QY 101 yAlaLysLysAspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSer 119
Db 363 TGCAGAAAGAGAGATTGACAGACCATAGTGAAGCATGCTCTGCTACT 417

RESULT 6
US-08-455-416-103
Sequence 103, Application US/08455416
Patent No. 5777200
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neunhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-455-416-103

Alignment Scores:
Pred. No.: 1,68e-54 Length: 653
Score: 445.00 Matches: 84
Percent Similarity: 84.87% Conservative: 17

```

Best Local Similarity: 70.59%      Mismatches: 17
Query Match: 72.36%      Indels: 1
DB: 1      Gaps: 0
US-09-786-715-6 (1-120) x US-08-455-416-103 (1-653)

QY 2 AlaglySerSerGluGluGlnValIleSerCysHisThrValGluGluTrpAsnAsp 21
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 63 GCTACTTCTCATCGAGGAGGACAGAGTTCGGCTGCCACAGAGTTGAGAAAGAGCGAG 122
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 22 GlnLeuGlnLysGlyAsnGlnSerLysLysLeuIleValValAspPheThrAlaSerTrp 41
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 123 TACTTCAGGAAAGGGGTTGAGACTGAAGAACTGGTGGTGCATTTTCTCTTCATCG 182
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 42 CysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSer 61
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 183 TCCGGSCCTTGGCCGTTTATTTCGCCCAATTCCTTGCTGACATTCGTAGAGAGATGCCCAT 242
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 62 ValIlePheLeuLysValAspValAspGluLeuLysSerValSerGlnAspTrpAlaIle 81
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 243 GTTATATTCCTCAGGTTGATGTGATGTAAGACTGAGAGACTGTTTCACGGGGAGATGAGTGT 302
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 81 eGluAlaMetProThrPheValPheValLysGlnGlyThrLeuLeuAspLysValValAla 101
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 303 GGAGGCAATGCCAAGCTTTTGTCTTCATTAAGATGGAAGAAAGAGTGACAGAGTGTGTGG 362
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 101 ValAlaLysAspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSer 119
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 363 TCCCAAGAAAGAGAGGAGTTGACGACAGACCATAGTGAAGCTGCTCTCTCTACT 417
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-08-455-244-103
; Sequence 103, Application US/08455244
; Patent No. 5789214
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericea C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,244
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/181,271

```

```

; FILING DATE: 13-JAN-94
; APPLICATION NUMBER: US 08/093,301
; FILING DATE: 16-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/937,197
; FILING DATE: 6-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/678,378
; FILING DATE: 1-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/305,566
; FILING DATE: 6-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/165,667
; FILING DATE: 8-MAR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-455-244-103

Alignment Scores:
Pred. No.: 1.68e-54      Length: 653
Score: 445.00      Matches: 84
Percent Similarity: 84.87%      Conservative: 17
Best Local Similarity: 70.59%      Mismatches: 17
Query Match: 72.36%      Indels: 1
DB: 1      Gaps: 0
US-09-786-715-6 (1-120) x US-08-455-244-103 (1-653)

QY 2 AlaglySerSerGluGluGlnValIleSerCysHisThrValGluGluTrpAsnAsp 21
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 63 GCTACTTCTCATCGAGGAGGACAGAGTTCGGCTGCCACAGAGTTGAGAAAGAGCGAG 122
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 22 GlnLeuGlnLysGlyAsnGlnSerLysLysLeuIleValValAspPheThrAlaSerTrp 41
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

Db 123 TACTTCAAGAAAGCGCTTGAAGAACTGGGTGGTGCATTTTACTGCTCAAGG 182
Qy 42 CysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSer 61
Db 183 TGCAGGCGCTTGCCTTTTATTGCCCCCAATTCCTGTCATGCTAAGAAATGCCCCAT 242
Qy 62 ValIlePheLeuLysValAspValAspGluLeuLysSerValSer-GlnAspTrpAlaIle 81
Db 243 GTTATATTCCTCAAGGTTGATGATGATGAACTGTTTCAAGCGGAAATGAGAGTGT 302
Qy 81 eGluAlaMetProThrPheValAlaPheValLysGluGlyThrLeuLeuAspLysValAlaGlu 101
Db 303 GGAAGCAATGCCAATCTTTGCTTCATTAAGATGAAAGAAAGTGCAGACAGTGTGG 362
Qy 101 YAlaLysLysAspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSer 119
Db 363 TGCAGAAAGAGAGGATTGCAGACCAATAGTGAAGCATGCTGCTCTGCTACT 417

```

RESULT 8

```

US-08-454-876-103
Sequence 103: Application US/08454876
Patent No. 5804693

```

GENERAL INFORMATION:

```

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Melns, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericea C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566

```

```

FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-454-876-103

```

Alignment Scores:

```

Pred. No.: 1.68e-54 Length: 653
Score: 445.00 Matches: 84
Percent Similarity: 84.87% Conservative: 17
Best Local Similarity: 70.59% Mismatches: 17
Query Match: 72.36% Indels: 1
DB: 1 Gaps: 0

```

```

US-09-786-715-6 (1-120) x US-08-454-876-103 (1-653)

```

```

Qy 2 AlaGlySerGluGluGlyGlnValIleSerCysHisThrValGluGluTrpAsp 21
Db 63 GCTACTTCATCCGAGGAGGCGCAAGTGTCCGCTGCCCAAGATTGAGATGACAG 122
Qy 22 GlnLeuGlnLysGlyAsnGluSerLysLysLeuIleValValAspPheThrAlaSer 41
Db 123 TACTTCAAGAAAGCGCTTGAAGAACTGGGTGGTGCATTTTACTGCTCAAGG 182
Qy 42 CysGlyProCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSer 61
Db 183 TGCAGGCGCTTGCCTTTTATTGCCCCCAATTCCTGTCATGCTAAGAAATGCCCCAT 242
Qy 62 ValIlePheLeuLysValAspValAspGluLeuLysSerValSer-GlnAspTrpAlaIle 81
Db 243 GTTATATTCCTCAAGGTTGATGATGATGAACTGTTTCAAGCGGAAATGAGAGTGT 302

```

```

OY      8  :=====ProthrinPhavalPhavalysglnglythrleuenukslysva1Valgl 101
Db      303 GGAGGCAATGCCACTTTGTCTTATTATTAAGATGGAAGAAAGATGACAGATTGTGG 362
OY      101 yalalytlyaspgluleuenglnlyslleclnlyshlsva1alaseralaser 119
Db      363 TGCCAGAAAGAGAGATTGTCACGACAGACATAGTGAAGCATGCTGCTCGTACT 417

RESULT 9
US-08-457-364-103
: Sequence 103, Application US/08457364
: Patent No. 5847258
: GENERAL INFORMATION:
: APPLICANT: Ryals, John A.
: APPLICANT: Alexander, Danny C.
: APPLICANT: Beck, James J.
: APPLICANT: Duesling, John H.
: APPLICANT: Friedrich, Leslie B.
: APPLICANT: Goodman, Robert M.
: APPLICANT: Harms, Christian
: APPLICANT: Meins, Jr., Frederick
: APPLICANT: Montoya, Alice
: APPLICANT: Moyer, Mary B.
: APPLICANT: Neuhaus, Jean-Marc
: APPLICANT: Payne, George B.
: APPLICANT: Sperison, Christoph
: APPLICANT: Stinson, Jeffrey R.
: APPLICANT: Utnes, Scott J.
: APPLICANT: Ward, Eric R.
: APPLICANT: Williams, Sheriecca C.
: TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
: TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
: NUMBER OF SEQUENCES: 106
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CIBA-GEIGY Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: New York
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/457,364
: FILING DATE: 31-MAY-1995
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/181,271
: FILING DATE: 13-JAN-94
: APPLICATION NUMBER: US 08/093,301
: FILING DATE: 16-JUL-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/937,197
: FILING DATE: 6-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/678,378
: FILING DATE: 1-APR-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/305,566
: FILING DATE: 6-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/165,667
: FILING DATE: 8-MAR-1988
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/042,847
: FILING DATE: 6-APR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/632,441
: FILING DATE: 21-DEC-1990
: PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEO ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-457-364-103

Alignment Scores:
Pred. No.: 1.68e-54 Length: 653
Score: 445.00 Matches: 84
Percent Similarity: 84.87% Conservative: 17
Best local Similarity: 70.59% Mismatches: 17
Query Match: 72.36% Indels: 1
DB: 2 Gaps: 0

US-09-786-715-6 (1-120) x US-08-457-364-103 (1-653)
QY 2 AAlGlySerSerIunGlunGIynValIIeserCySHstHrVnAlGlunGIutPrAsp 21
   |  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 63 GcACTTCAATCCAGGAGGGACAAAGTGTTGGCGTCGCCAACGAAGTTGAGAGTAAGCAG 122
   |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 22 GlLueGlnInISglSngInUserIySLysLeuIlleValIaASpphetHraLaSerTrp 41
   :  :::::  |||  :::::  |||||  |||||  |||||  |||||  |||||  |||||
Db 123 TACTTCAAGAAGAGCGCTTAGAGACTAAGAAACGTGGGTGGTGCATTTTACTGCTCATGG 182
   :  :::::  |||  :::::  |||||  |||||  |||||  |||||  |||||  |||||

QY 42 CysGLyProCysArpHeIIeaIaProheleuaIaGluleuaIaLySLysPheThrSer 61
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 183 TCGGSGCCTTCGCGTTTATTCGCCCAATTTCTTGCTGACATTTCTAAGAAGATCCCCAT 242
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 62 ValIIePheleuLySaIaSpYaIaSpGUleuLySSerVaISeR-GlnasPrtpIaail 81
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 243 GTTATATTCCTCAAGGTGATGTTGATGAAGAACTGAAGACTGTTTCAGCGGAATGAGCTGT 302
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 81 egiuaIameProThrPheValPheValISglunGIythrIeuuaSplySaIaIgl 101
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 303 GGAGGCAATGCCCACTTTGTCTTCATTAAAGATGGAATAAAGTGCACAGATGTTGG 362
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 101 yalaLyLSaSpgLUleuGlnGlnISylleGlnIyShISaIaASeraIaser 119
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 363 TGCCAAGAAAAGAGAGTTCACACAGACATAGTGAAGCATGCTCTCCTCTACT 417
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 10
US-08-456-262-103
Sequence 103, Application US/08455262
```

Patent No. 5851766
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neunus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Spertson, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,262
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PI/CCG 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SRO ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-456-262-103
Alignment Scores:
Pred. No.: 1.68e-54 Length: 653
Score: 445.00 Matches: 84
Percent Similarity: 84.87% Conservative: 17
Best Local Similarity: 70.59% Mismatches: 17
Query Match: 72.36% Indels: 1
Gaps: 0
US-09-786-715-6 (1-120) x US-08-456-262-103 (1-653)
QY 2 Alaglysersegluglglglnvalillessercyhsithryvalgluglutrpsanasp 21
Db 63 GCTACTTCATCCAGGAGGCGACCAAGTGGCTGCCACCAAGTGGAGTGAACGAG 122
QY 22 Glnleuglnlysgllyansgluserlyslsleuilevalvalasppherhrlasertrp 41
Db 123 TACTTCAGAAAGCCGTTGAGACTAGAAACTGCTGCTGCTTACTGCTTATGCG 182
QY 42 CysglpProcysarpheliealaProphelueuAgluAgluAgluAgluAgluAglu 61
Db 183 TGGGSGCCTTCCGCTTTATTTGCCCCAATTCCTGCTGACATCTGCTAAGAAAGTCCCAT 242
QY 62 Valillepheleulysvalasppvalasppgluleulyssevalser-Glnaspptrpalail 81
Db 243 GTTATATTCCTCAAGGTGATGTTGATGAGACTGAGACTGTTTCAGGGGAATGAGGTGT 302
QY 81 egluAlaMetProThrPheValPheValIlysglgluGlyThrLeuLeuAspIlyValI 101
Db 303 GGAAGCAATGCCAAGCTTTTGTCTTCATTAAAGATGCAAAAGAGTGACAGATGTTGG 362
QY 101 yAlaLylysAspGluleuglnInlyslleglnTylshIsvalAlaserAlaser 119
Db 363 TGGCAAGAAAGAGAGAGTTCGACGACACCAATAGGAGCAATGCGTCTCTCTACT 417
RESULT 11
US-08-456-240-103
Sequence 103, Application US/08456240
Patent No. 5856154
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice

REGISTRATION NUMBER: 36,129	
REFERENCE/DOCKET NUMBER: S-19825/91/CGC 1727	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: (919)541-8614	
TELEFAX: (919)541-8689	
INFORMATION FOR SEQ ID NO: 103:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 653 base pairs	
TYPE: nucleic acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: DNA (genomic)	
US-08-456-240-103	
Alignment Scores:	
Pred. No.: 1,68e-54	Length: 653
Score: 445.00	Matches: 84
Percent Similarity: 84.87%	Conservative: 17
Best Local Similarity: 70.59%	Mismatches: 17
Query Match: 72.36%	Indels: 1
DB: 2	Gaps: 0
US-09-786-715-6 (1-120) x US-08-456-240-103 (1-653)	
QY	2
63	63
22	22
123	123
QY	42
183	183
QY	62
243	243
Db	81
303	303
QY	101
363	363
RESULT 12	
US-08-453-736-103	
Sequence 103, Application US/08455736	
Patent No. 5880328	
GENERAL INFORMATION:	
APPLICANT: Ryals, John A.	
APPLICANT: Alexander, Danny C.	
APPLICANT: Beck, James J.	
APPLICANT: Duesling, John H.	
APPLICANT: Friedrich, Leslie B.	
APPLICANT: Goodman, Robert M.	
APPLICANT: Harms, Christian	
APPLICANT: Weins, Jf., Frederick	
APPLICANT: Montoya, Alice	
APPLICANT: Moyer, Mary B.	
APPLICANT: Neuhaus, Jean-Marc	
APPLICANT: Payne, George B.	
APPLICANT: Sperison, Christoph	
APPLICANT: Stinson, Jeffrey R.	
APPLICANT: Uknes, Scott J.	
APPLICANT: Ward, Eric R.	
APPLICANT: Williams, Sherica C.	
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC	
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF	
NUMBER OF SEQUENCES: 106	


```

Db      123 TACTTCAGAAAGCGGCTTGAGACTAAGAAACGTGGTGGTGCATTTTACTGCTTCATGG 182
QY      42 CYSGLYPRCCysArgPheIleAlaProPheLeuAlaGluLeuAlaLysLysPheThrSer 61
       183 TGGGCGCCTTGGCGGCTTTTATTGCCCCCACTTCTGCTGACATGTGTAAGAAAGATCCCCAT 242
QY      62 ValIlePheLeuLeuValAspValAspGluLeuLysSerValSer-GlnAspTPAlaIle 81
       243 GTATATATTCCTCAAGGCTGATCTTGATATGATCACTGAAGACCTGTTTCAAGGGGAATGAGTGT 302
QY      81 egttAlaMetProThrPheValPheValLysGluGlyThrLeuLeuAspLysValValGI 101
       Db      303 GGAGCGAATGCCAACACTTTTGTCTTCTTCATTAAAGATGGAAGAAAGAAATGACAGAGTGTGG 362
QY      101 yAlaLysLysAspGluLeuGlnGlnLysIleGlnLysHisValAlaSerAlaSer 119
       Db      363 TGCCAGAAAGAGAGAGGATTGACACGACACATAGTGAGCATGCTGCTCTGCTACT 417
RESULT 14
US-09-350-600-103
Sequence 103, Application US/09350600
Patent No. 6262342
GENERAL INFORMATION:
APPLICANT: Meins, Frederick
APPLICANT: Shinshu, Hideaki
APPLICANT: Wenzler, Herman
APPLICANT: Hofsteenge, Jan
APPLICANT: Ryals, John
APPLICANT: Spertsen, Christoph
TITLE OF INVENTION: DNA SEQUENCES ENCODING POLYPEPTIDES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6262342artis Corporation
STREET: 3054 Cornwallis Road, P.O. Box 12257
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,600
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/971,217
FILING DATE: 14-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,364
FILING DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847

```

FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/381,443
FILING DATE: 18-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/353,312
FILING DATE: 17-MAY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/226,303
FILING DATE: 29-JUL-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-198250
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-350-600-103

Alignment Scores:
Pred. No.: 1.68e-54 Length: 653
Score: 445.00 Matches: 84
Percent Similarity: 84.87% Conservative: 17
Best Local Similarity: 70.59% Mismatches: 17
Query Match: 72.36% Indels: 1
Gaps: 0

US-09-786-715-6 (1-120) x US-09-350-600-103 (1-653)

QY 2 AlaglyserSerIugluIugIvalIleserCysHisThrValaIugluIutPrasnAsp 21
Db 63 GCTACTTCATCCAGGAGGAGCAAGTGTGGCTGCCACCAAGTGTGAGATGGACGAC 122
QY 22 GlnleuGlnLysgluLysleuSerLysLysleuIleValaValaspphetrAlaSerTrp 41
Db 123 TACTTCAGAAAGCGCTGTGAGACTAGAAACTGCTGTGCTTACTTCTTCATGG 182
QY 42 CysglYProCysArgPheIleAlaProPheLeuAlaIuValaLysLysPheThrSer 61
Db 183 TGGGSCCTTGCGCTTTATTTGCCCAATCTTGTCACATGTGTAAGAGATGCCCAT 242
QY 62 ValIlePheLeuLysValaValaspphetrAlaSerGlnasptRpAlaIle 81

|||||
Db 243 GTTATATTCCTCAAGGTGTGATGTGATGAAGACTGTTTCACGGCAATGAGTGT 302
QY 81 egluAlaMetProThrPheValaIleValaLysgluIYThrLeuAspLysValaIle 101
Db 303 GGAGGCATGTGCAACTTTTGTCTTCATTAAGATGAAAGAGATGGACAGATGTGG 362
QY 101 YAlaLysLysAspGluLeuGlnGlnLysIleGlnLysHisValaLaserAlaSer 119
Db 363 TGCCAGAGAGAGAGAGTGTGACGACACCATATGTAAGACATGCTCTCTACT 417

RESULT 15
US-09-540-014-5
Sequence 5, Application US/09540014
Patent No. 6380372
GENERAL INFORMATION:
APPLICANT: Cho, Myeong-Je
APPLICANT: Del Val, Greg
APPLICANT: Lemauz, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: Barley Gene for Thioresoxin and
TITLE OF INVENTION: NADP-Thioresoxin Reductase
FILE REFERENCE: 2001-0701.30
CURRENT FILING DATE: US/09/540,014
PRIOR APPLICATION NUMBER: US 60/127,198
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US 60/169,162
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,739
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 393
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: wheat thioresoxin h cDNA
US-09-540-014-5

Alignment Scores:
Pred. No.: 8.65e-44 Length: 393
Score: 368.00 Matches: 63
Percent Similarity: 81.82% Conservative: 27
Best Local Similarity: 57.27% Mismatches: 20
Query Match: 59.84% Indels: 0
Gaps: 0

US-09-786-715-6 (1-120) x US-09-540-014-5 (1-393)

QY 8 GlnGlnValIleSerCysHisThrValaIugluIutPrasnAspGlnleuGlnLysglu 27
Db 61 GGGAGGTGATCTCCGTCACAGCCTGACAGCAGTGCATGCAGATCGAGGAGCCAC 120
QY 28 GluSerLysLysleuIleValaValaspphetrAlaSerTrpCysglYProCysArgPhe 47
Db 121 GCCGCCAAGAGCTGGTGGTGTGATGTGATCTTACTGACATGATGCGGACCATGCCG 180
QY 48 IleAlaProPheLeuAlaIuValaLysLysPheThrSerValIlePheLeuVala 67
Db 181 ATGGCTCCATTTTGTGATCTGCGCAAGATGCCACCTGCTGTTCCTCAAGTTC 240
QY 68 AspValaLysgluLeuLysSerValSerGlnasptRpAlaIleGluAlaMetProThrPhe 87
Db 241 GACGTTGATGAATGAAAGCCCATGTCGACCAATTCAGCTCGAGGCGCATGCCAACCCTTC 300
QY 88 ValPheValLysgluIugluIYThrLeuLeuAspLysValaIleGlnLysLysAspGlu 107
Db 301 CTGTTCATGTAAGAGAGAGACGTCAAGACAGGAGTGTGAGACTATCAAGAGAGACTG 360

OY 108 GlnGlnLysIleGlnLysHisValAlaSer 117
|||::|
Db 361 ACGACCAAGGTGGGCTCCACGCGGCTGCC 390

Search completed: August 17, 2003, 21:45:22
Job time : 53.472 secs